

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2004, 15:30:06 ; Search time 43.3077 Seconds
(without alignments)
71.766 Million cell updates/sec

Title: US-09-787-443A-2
Perfect score: 11
Sequence: 1 AKKERQRKDTQ 11

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1586107 seqs, 282547505 residues

Word size : 0

Total number of hits satisfying chosen parameters: 22883

Minimum DB seq length: 11

Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	11	100.0	11	3	AAy88528	Aay88528 NCAM Ig1
2	11	100.0	11	3	AAy88561	Aay88561 NCAM Ig1
3	11	100.0	11	5	ABG69330	Abg69330 Human neu
4	4	36.4	11	2	AAR37430	Aar37430 Promega p
5	4	36.4	11	2	AAR96841	Aar96841 Human moe
6	4	36.4	11	2	AAW09653	Aaw09653 Labelled
7	4	36.4	11	2	AAW11749	Aaw11749 T-cell re
8	4	36.4	11	2	AAW11750	Aaw11750 T-cell re
9	4	36.4	11	2	AAy31014	Aay31014 Non-cross

10	4	36.4	11	3	AAy88545	Aay88545	NCAM Igl
11	4	36.4	11	4	ABP19679	Abp19679	HIV B62 s
12	4	36.4	11	4	ABP17507	Abp17507	HIV B27 s
13	4	36.4	11	4	ABP14260	Abp14260	HIV A02 s
14	4	36.4	11	4	ABP16618	Abp16618	HIV A24 s
15	4	36.4	11	4	ABP24378	Abp24378	HIV A24 m
16	4	36.4	11	4	ABP14259	Abp14259	HIV A02 s
17	4	36.4	11	4	ABP16617	Abp16617	HIV A24 s
18	4	36.4	11	4	ABP16616	Abp16616	HIV A24 s
19	4	36.4	11	5	ABG69345	Abg69345	Human neu
20	4	36.4	11	5	AAO18039	Aao18039	Human imm
21	3	27.3	11	1	AAP60142	Aap60142	Type 3 pe
22	3	27.3	11	1	AAP71164	Aap71164	Peptide w
23	3	27.3	11	1	AAP90643	Aap90643	Signal pe
24	3	27.3	11	2	AAR02183	Aar02183	Peptide w
25	3	27.3	11	2	AAR06031	Aar06031	Oligopept
26	3	27.3	11	2	AAR08092	Aar08092	Antifreez
27	3	27.3	11	2	AAR15673	Aar15673	Asn-resid
28	3	27.3	11	2	AAR12168	Aar12168	Neuropept
29	3	27.3	11	2	AAR12171	Aar12171	Neuropept
30	3	27.3	11	2	AAR12173	Aar12173	Neuropept
31	3	27.3	11	2	AAR22743	Aar22743	Non-A, No
32	3	27.3	11	2	AAR35381	Aar35381	Amphiphil
33	3	27.3	11	2	AAR32351	Aar32351	Human Fac
34	3	27.3	11	2	AAR33973	Aar33973	Amphiphil
35	3	27.3	11	2	AAR31163	Aar31163	C-termina
36	3	27.3	11	2	AAR34248	Aar34248	Mutant HT
37	3	27.3	11	2	AAR30442	Aar30442	Synthetic
38	3	27.3	11	2	AAR30463	Aar30463	Synthetic
39	3	27.3	11	2	AAR30478	Aar30478	Synthetic
40	3	27.3	11	2	AAR41495	Aar41495	TNF inhib
41	3	27.3	11	2	AAR39369	Aar39369	Human gly
42	3	27.3	11	2	AAR45132	Aar45132	Amphiphil
43	3	27.3	11	2	AAR34421	Aar34421	Hepatitis
44	3	27.3	11	2	AAR55163	Aar55163	Fragment
45	3	27.3	11	2	AAR50563	Aar50563	Amphiphil
46	3	27.3	11	2	AAR55987	Aar55987	Ion chann
47	3	27.3	11	2	AAR59065	Aar59065	Cancer tr
48	3	27.3	11	2	AAR56948	Aar56948	Peptide w
49	3	27.3	11	2	AAR50448	Aar50448	Amphiphil
50	3	27.3	11	2	AAR51276	Aar51276	Meningoco
51	3	27.3	11	2	AAR51277	Aar51277	Meningoco
52	3	27.3	11	2	AAR82678	Aar82678	V8 fragme
53	3	27.3	11	2	AAW21496	Aaw21496	Hepatitis
54	3	27.3	11	2	AAW21220	Aaw21220	Farnesyl
55	3	27.3	11	2	AAR76917	Aar76917	Thymosin
56	3	27.3	11	2	AAR84537	Aar84537	Hepatitis
57	3	27.3	11	2	AAR90259	Aar90259	Ion-chann
58	3	27.3	11	2	AAR91788	Aar91788	Ion-chann
59	3	27.3	11	2	AAR91787	Aar91787	Ion-chann
60	3	27.3	11	2	AAR87902	Aar87902	Neuropept
61	3	27.3	11	2	AAW49555	Aaw49555	Human leu
62	3	27.3	11	2	AAR96835	Aar96835	Human neu
63	3	27.3	11	2	AAR85318	Aar85318	Human ret
64	3	27.3	11	2	AAW18499	Aaw18499	Amino-ter
65	3	27.3	11	2	AAW24438	Aaw24438	Nucleic a
66	3	27.3	11	2	AAW34642	Aaw34642	Control p

67	3	27.3	11	2	AAW09909	Aaw09909 Prostate
68	3	27.3	11	2	AAW10140	Aaw10140 Hepatitis
69	3	27.3	11	2	AAW62116	Aaw62116 Human MDM
70	3	27.3	11	2	AAW66523	Aaw66523 Amphiphil
71	3	27.3	11	2	AAW80589	Aaw80589 src-famil
72	3	27.3	11	2	AAW64653	Aaw64653 Synthetic
73	3	27.3	11	2	AAW51825	Aaw51825 Peptide Y
74	3	27.3	11	2	AAW84029	Aaw84029 Human CYP
75	3	27.3	11	2	AAW84023	Aaw84023 Human CYP
76	3	27.3	11	2	AAW84026	Aaw84026 Human CYP
77	3	27.3	11	2	AAW50263	Aaw50263 HIV-1 tat
78	3	27.3	11	2	AAW30700	Aay30700 Apo-B100
79	3	27.3	11	2	AAW30698	Aay30698 Apo-B100
80	3	27.3	11	2	AAW72988	Aaw72988 Bovine be
81	3	27.3	11	2	AAW05150	Aay05150 HIV Tat p
82	3	27.3	11	2	AAW39666	Aay39666 Tat-inhib
83	3	27.3	11	2	AAW39664	Aay39664 Tat-inhib
84	3	27.3	11	2	AAW39667	Aay39667 Tat-inhib
85	3	27.3	11	2	AAW39662	Aay39662 Tat-inhib
86	3	27.3	11	2	AAW39663	Aay39663 Tat-inhib
87	3	27.3	11	2	AAW39665	Aay39665 Tat-inhib
88	3	27.3	11	2	AAW39669	Aay39669 Tat-inhib
89	3	27.3	11	2	AAW97477	Aaw97477 Antigenic
90	3	27.3	11	2	AAW05415	Aay05415 Tat pepti
91	3	27.3	11	2	AAW81004	Aaw81004 S. cerevi
92	3	27.3	11	2	AAW05440	Aay05440 Bronchodi
93	3	27.3	11	2	AAW25084	Aay25084 TAT domai
94	3	27.3	11	2	AAW25075	Aay25075 TAT trans
95	3	27.3	11	2	AAW10761	Aay10761 Peptide u
96	3	27.3	11	2	AAW10750	Aay10750 Peptide u
97	3	27.3	11	2	AAW10762	Aay10762 Peptide u
98	3	27.3	11	3	AAW66823	Aay66823 T cell an
99	3	27.3	11	3	AAW27088	Aab27088 Beta-cate
100	3	27.3	11	3	AAW16472	Aab16472 Linear pe

ALIGNMENTS

RESULT 1

AAW88528

ID AAW88528 standard; peptide; 11 AA.

XX

AC AAW88528;

XX

DT 07-AUG-2000 (first entry)

XX

DE NCAM Igl binding peptide D3.

XX

KW NCAM; neural cell adhesion molecule; Igl; immunoglobulin domain 1;

KW neurite outgrowth promoter; proliferation; nerve damage; sclerosis;

KW impaired myelination; stroke; Parkinson's disease; memory; schizophrenia;

KW Alzheimer's disease; diabetes mellitus; circadian clock; nephrosis;

KW treatment; prosthetic nerve guide; treatment; nervous system.

XX

OS Synthetic.

XX

PN WO200018801-A2.
XX
PD 06-APR-2000.
XX
PF 23-SEP-1999; 99WO-DK000500.
XX
PR 29-SEP-1998; 98DK-00001232.
PR 29-APR-1999; 99DK-00000592.
XX
PA (RONN/) RONN L C B.
PA (BOCK/) BOCK E.
PA (HOLM/) HOLM A.
PA (OLSE/) OLSEN M.
PA (OSTE/) OSTERGAARD S.
PA (JENS/) JENSEN P H.
PA (POUL/) POULSEN F M.
PA (SORO/) SOROKA V.
PA (RALE/) RALETS I.
PA (BERE/) BEREZIN V.
XX
PI Ronn LCB, Bock E, Holm A, Olsen M, Ostergaard S, Jensen PH;
PI Poulsen FM, Soroka V, Ralets I, Berezin V;
XX
DR WPI; 2000-293111/25.
XX
PT Compositions that bind neural cell adhesion molecules useful for treating
PT disorders of the nervous system and muscles e.g. Alzheimer's and
PT Parkinson's diseases.
XX
PS Claim 20; Page 82; 119pp; English.
XX
CC Neural cell adhesion molecule (NCAM) is a cellular adhesion molecule.
CC NCAM is found in three forms, two of which are transmembrane forms, while
CC the third is attached via a lipid anchor to the cell membrane. All three
CC NCAM forms have an extracellular structure consisting five immunoglobulin
CC domains (Ig domains). The Ig domains are numbered 1 to 5 from the N-
CC terminal. The present sequence represents a peptide which binds to the
CC NCAM Ig1 domain. The peptide can be used in a compound which binds to
CC NCAM-Ig1/Ig2 domains, and is capable of stimulating or promoting neurite
CC outgrowth from NCAM presenting cells, and is also capable of promoting
CC the proliferation of NCAM presenting cells. The compound may be used in
CC the treatment of normal, degenerated or damaged NCAM presenting cells.
CC The compound may in particular be used to treat diseases of the central
CC and peripheral nervous systems such as post operative nerve damage,
CC traumatic nerve damage, impaired myelination of nerve fibres, conditions
CC resulting from a stroke, Parkinson's disease, Alzheimer's disease,
CC dementias, sclerosis, nerve degeneration associated with diabetes
CC mellitus, disorders affecting the circadian clock or neuro-muscular
CC transmission and schizophrenia. Conditions affecting the muscles may also
CC be treated with the compound, such as conditions associated with impaired
CC function of neuromuscular connections (e.g. genetic or traumatic shock or
CC traumatic atrophic muscle disorders). Conditions of the gonads, pancreas
CC (e.g. diabetes mellitus types I and II), kidney (e.g. nephrosis), heart,
CC liver and bowel may also be treated using the compound. The compound is
CC used in a prosthetic nerve guide, and also to stimulate the ability to
CC learn, and to stimulate the memory of a subject
XX

SQ Sequence 11 AA;

Query Match 100.0%; Score 11; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKKERQRKDTQ 11
| | | | | | | | | |
Db 1 AKKERQRKDTQ 11

RESULT 2

AAAY88561

ID AAY88561 standard; peptide; 11 AA.

XX

AC AAY88561;

XX

DT 07-AUG-2000 (first entry)

XX

DE NCAM Igl binding peptide D3 used as a control peptide.

XX

KW NCAM; neural cell adhesion molecule; Igl; immunoglobulin domain 1;

KW neurite outgrowth promoter; proliferation; nerve damage; sclerosis;

KW impaired myelination; stroke; Parkinson's disease; memory; schizophrenia;

KW Alzheimer's disease; diabetes mellitus; circadian clock; nephrosis;

KW treatment; prosthetic nerve guide; treatment; nervous system.

XX

OS Synthetic.

XX

PN WO200018801-A2.

XX

PD 06-APR-2000.

XX

PF 23-SEP-1999; 99WO-DK000500.

XX

PR 29-SEP-1998; 98DK-00001232.

PR 29-APR-1999; 99DK-00000592.

XX

PA (RONN/) RONN L C B.

PA (BOCK/) BOCK E.

PA (HOLM/) HOLM A.

PA (OLSE/) OLSEN M.

PA (OSTE/) OSTERGAARD S.

PA (JENS/) JENSEN P H.

PA (POUL/) POULSEN F M.

PA (SORO/) SOROKA V.

PA (RALE/) RALETS I.

PA (BERE/) BEREZIN V.

XX

PI Ronn LCB, Bock E, Holm A, Olsen M, Ostergaard S, Jensen PH;

PI Poulsen FM, Soroka V, Ralets I, Berezin V;

XX

DR WPI; 2000-293111/25.

XX

PT Compositions that bind neural cell adhesion molecules useful for treating

PT disorders of the nervous system and muscles e.g. Alzheimer's and

PT Parkinson's diseases.

XX
 PS Example 5; Fig 7; 119pp; English.
 XX
 CC Neural cell adhesion molecule (NCAM) is a cellular adhesion molecule.
 CC NCAM is found in three forms, two of which are transmembrane forms, while
 CC the third is attached via a lipid anchor to the cell membrane. All three
 CC NCAM forms have an extracellular structure consisting five immunoglobulin
 CC domains (Ig domains). The Ig domains are numbered 1 to 5 from the N-
 CC terminal. The invention relates to a compound containing a peptide which
 CC binds to the NCAM Ig1 domain. The compound binds to NCAM-Ig1/Ig2 domains,
 CC and is capable of stimulating or promoting neurite outgrowth from NCAM
 CC presenting cells, and is also capable of promoting the proliferation of
 CC NCAM presenting cells. The present sequence represents a control peptide
 CC used in the identification of those binding peptides which can be used in
 CC the compound. The compound may be used in the treatment of normal,
 CC degenerated or damaged NCAM presenting cells. The compound may in
 CC particular be used to treat diseases of the central and peripheral
 CC nervous systems such as post operative nerve damage, traumatic nerve
 CC damage, impaired myelination of nerve fibres, conditions resulting from a
 CC stroke, Parkinson's disease, Alzheimer's disease, dementias, sclerosis,
 CC nerve degeneration associated with diabetes mellitus, disorders affecting
 CC the circadian clock or neuro-muscular transmission and schizophrenia.
 CC Conditions affecting the muscles may also be treated with the compound,
 CC such as conditions associated with impaired function of neuromuscular
 CC connections (e.g. genetic or traumatic shock or traumatic atrophic muscle
 CC disorders). Conditions of the gonads, pancreas (e.g. diabetes mellitus
 CC types I and II), kidney (e.g. nephrosis), heart, liver and bowel may also
 CC be treated using the compound. The compound is used in a prosthetic nerve
 CC guide, and also to stimulate the ability to learn, and to stimulate the
 CC memory of a subject
 XX
 SQ Sequence 11 AA;

Query Match 100.0%; Score 11; DB 3; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.3e-05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKKERQRKDTQ 11
 |||||
 Db 1 AKKERQRKDTQ 11

RESULT 3
 ABG69330
 ID ABG69330 standard; peptide; 11 AA.
 XX
 AC ABG69330;
 XX
 DT 21-OCT-2002 (first entry)
 XX
 DE Human neural cell adhesion molecule (NCAM) peptide #2.
 XX
 KW Human; neural cell adhesion molecule; NCAM; heart muscle cell survival;
 KW acute myocardial infarction; central nervous system disorder; stroke;
 KW peripheral nervous system disorder; postoperative nerve damage;
 KW traumatic nerve damage; spinal cord injury; nerve fibre; schizophrenia;
 KW postischaemic damage; multiinfarct dementia; multiple sclerosis;

KW nerve degeneration; diabetes mellitus; neuro-muscular degeneration;
 KW Alzheimer's disease; Parkinson's disease;
 KW Huntington's disease. atrophic muscle disorder; gonad degeneration;
 KW nephrosis.
 XX
 OS Homo sapiens.
 XX
 PN WO200247719-A2.
 XX
 PD 20-JUN-2002.
 XX
 PF 12-DEC-2001; 2001WO-DK000822.
 XX
 PR 12-DEC-2000; 2000DK-00001863.
 XX
 PA (ENKA-) ENKAM PHARM AS.
 XX
 PI Bock E, Berezin V, Kohler LB;
 XX
 DR WPI; 2002-583473/62.
 XX
 PT Use of a compound comprising a peptide of neural cell adhesion molecule,
 PT in the preparation of medicament for preventing death of cells presenting
 PT NCAM or NCAM ligand and treating central nervous system diseases.
 XX
 PS Claim 26; Page 39; 57pp; English.
 XX
 CC The invention relates to use of a compound (I) comprising a peptide which
 CC comprises at least 5 contiguous amino acid residues of a sequence of the
 CC neural cell adhesion molecule (NCAM), its fragment, variant or its mimic,
 CC for the preparation of a medicament for preventing death of cells
 CC presenting the NCAM or an NCAM ligand. (I) is useful in the preparation
 CC of a medicament for preventing death of cells presenting the NCAM or an
 CC NCAM ligand. The medicament is for the stimulation of the survival of
 CC heart muscle cells, such as survival after acute myocardial infarction.
 CC The medicament is for the treatment of diseases or conditions of the
 CC central and peripheral nervous system, such as postoperative nerve
 CC damage, traumatic nerve damage, e.g. resulting from spinal cord injury,
 CC impaired myelination of nerve fibres, postischaemic damage, e.g.
 CC resulting from a stroke, multiinfarct dementia, multiple sclerosis, nerve
 CC degeneration associated with diabetes mellitus, neuro-muscular
 CC degeneration, schizophrenia, Alzheimer's disease, Parkinson's disease and
 CC Huntington's disease. The medicament is for the treatment of diseases or
 CC conditions of the muscles including conditions with impaired function of
 CC neuro-muscular connections, such as genetic or traumatic atrophic muscle
 CC disorders, and for the treatment of diseases or conditions of various
 CC organs, such as degenerative conditions of the gonads, pancreas (e.g.
 CC diabetes mellitus type I and II) and kidney (e.g. nephrosis). ABG69329-
 CC ABG69352 represent human NCAM peptides of the invention
 XX
 SQ Sequence 11 AA;

Query Match 100.0%; Score 11; DB 5; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.3e-05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKKERQQRKDTQ 11

Db |||||
1 AKKERQRKDTQ 11

RESULT 4

AAR37430

ID AAR37430 standard; peptide; 11 AA.

XX

AC AAR37430;

XX

DT 25-MAR-2003 (revised)

DT 08-SEP-1993 (first entry)

XX

DE Promega peptide 5.

XX

KW Modified peptide substrate; non-radioactive; detection; dansyl;
KW sulphorhodamine 101; lissamine; rhodamine; enzymes; phosphatases;
KW protein kinases; proteases.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

/note= "detection tag= lissamine, Rhodamine"

XX

PN WO9310461-A1.

XX

PD 27-MAY-1993.

XX

PF 12-NOV-1992; 92WO-US009595.

XX

PR 12-NOV-1991; 91US-00791928.

XX

PA (PROM-) PROMEGA CORP.

XX

PI Shultz JW, White DH;

XX

DR WPI; 1993-182698/22.

XX

PT Quantitating presence or activity of enzyme - by incubating with modified
PT peptide substrate and measuring the modified peptide prod.

XX

PS Claim 24; Page 27; 103pp; English.

XX

CC Promega peptide 5 is tagged with dansyl at residue 1 and may be used in a
CC novel non-radioactive method of quantitating the presence or activity of
CC an enzyme. The method can be used for rapid, specific and highly
CC sensitive detection of enzymes such as protein kinases, phosphatases and
CC proteases, esp. in this case protein kinase C. They can be used to study
CC enzyme function in metabolism and in diagnosis of disease. They also
CC allow quantitative determ. of the enzyme's activity. See also AAR37426-
CC 36. (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 8.2e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQRK 8
| | | |
Db 3 RQRK 6

RESULT 5

AAR96841

ID AAR96841 standard; peptide; 11 AA.

XX

AC AAR96841;

XX

DT 29-NOV-1996 (first entry)

XX

DE Human moesin fragment, homologous to Neisseria Iga-alpha2.

XX

KW IgA protease precursor; IPP; bacterial polyprotein; autoimmune;

KW viral infection; rheumatoid arthritis; AIDS; meningococcal bacteria;

KW human small nuclear ribonucleoprotein-associated protein; Rsmb;

KW Neisseria gonorrhoeae; R16.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Region 1

FT /note= "identical to corresponding residue in Neisseria
FT gonorrhoeae Iga-alpha2"

FT Region 6. .11

FT /note= "identical to sequence in Neisseria gonorrhoeae
FT Iga-alpha2"

XX

PN WO9609395-A2.

XX

PD 28-MAR-1996.

XX

PF 21-SEP-1995; 95WO-EP003726.

XX

PR 21-SEP-1994; 94DE-04433708.

XX

PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.

XX

PI Meyer TF, Pohlner J, Beck SC, Jose J, Woelk U, Lorenzen DR;

PI Oetzelberger KB;

XX

DR WPI; 1996-188456/19.

XX

PT Medicaments for treating auto-immune or viral diseases - contg.

PT substances interfering with bacterial poly:protein function.

XX

PS Claim 32; Fig 2; 117pp; German.

XX

CC The present sequence from human moesin has homology to a cleavage product
CC from the Iga-alpha2 domain of the precursor of IgA-protease polyprotein
CC (IPP) of Neisseria gonorrhoeae strain R16. The Neisseria IPP has been
CC implicated in rheumatoid arthritis and other auto-immune diseases. The
CC polyprotein also activates proviruses, including HIV. Substances which

CC interfere with the function of IPP from Neisseria will be useful for
CC treating associated autoimmune diseases and viral infections. Peptides
CC comprising the homology region sequences, whether from Neisseria or from
CC humans, are claimed
XX
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KERQ 6
 ||||
Db 2 KERQ 5

RESULT 6

AAW09653

ID AAW09653 standard; peptide; 11 AA.

XX

AC AAW09653;

XX

DT 25-MAR-2003 (revised)

DT 20-MAY-1997 (first entry)

XX

DE Labelled peptide substrate used in enzyme activity assay.

XX

KW Enzyme activity; assay; measurement; label; rhodamine; dansyl;

KW non-radioactive; electrophoretic separation; protein kinase; protease;

KW phosphatase.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "labelled with rhodamine B detection tag"

XX

PN US5580747-A.

XX

PD 03-DEC-1996.

XX

PF 21-JAN-1994; 94US-00185448.

XX

PR 12-NOV-1991; 91US-00791928.

XX

PA (PROM-) PROMEGA CORP.

XX

PI White DH, Shultz JW;

XX

DR WPI; 1997-033568/03.

XX

PT Non:radioactive assay for measuring enzyme activity - involving

PT electrophoretic sepn. of labelled cleavage prod. from labelled peptide

PT substrate.

XX

PS Claim 5; Col 39-40; 35pp; English.

XX

CC AAW09653 is a peptide substrate used in a non-radioactive assay for
CC measuring enzyme activity. The assay comprises incubating the enzyme with
CC the labelled peptide substrate to form a labelled peptide product;
CC separating the product from the substrate by agarose gel electrophoresis
CC and measuring the amount of product by detecting the label by
CC fluorescence or chemiluminescence. The assay can be performed rapidly and
CC with great sensitivity. This peptide is especially for determining
CC protein kinase C activity, e.g. to study its function in metabolism or to
CC screen for potential inhibitors. (Updated on 25-MAR-2003 to correct PF
CC field.)

XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQRK 8

||||

Db 3 RQRK 6

RESULT 7

AAW11749

ID AAW11749 standard; peptide; 11 AA.

XX

AC AAW11749;

XX

DT 04-NOV-1997 (first entry)

XX

DE T-cell receptor peptide V(beta)5.2 (49-59)F.

XX

KW T-cell receptor; TCR; V(beta)5.2; multiple sclerosis;

KW rheumatoid arthritis; myasthenia gravis; encephalomyelitis; diabetes;

KW inflammatory bowel disease; systemic lupus erythematosus; thyroiditis;

KW therapy; diagnosis; vaccine.

XX

OS Synthetic.

XX

PN WO9640778-A1.

XX

PD 19-DEC-1996.

XX

PF 06-JUN-1996; 96WO-US009423.

XX

PR 07-JUN-1995; 95US-00476405.

XX

PA (CONN-) CONNECTIVE THERAPEUTICS INC.

XX

PI Vandembark AA;

XX

DR WPI; 1997-099923/09.

XX

PT T cell receptor peptide derived from V(beta)-5 family - useful for
PT treating e.g. multiple sclerosis, myasthenia gravis, diabetes, etc.

XX

PS Claim 9; Page 42; 54pp; English.

XX
CC This sequence is a synthetic peptide based on amino acid residues 49-59
CC of the V(beta)5.2 region (see AAW11767) of human T cell receptor (TCR).
CC It is a specifically preferred peptide for use in a claimed method for
CC the treatment, prevention or suppression of a T-cell mediated disease
CC such as multiple sclerosis, rheumatoid arthritis, myasthenia gravis,
CC encephalomyelitis, thyroiditis, diabetes, inflammatory bowel disease or
CC systemic lupus erythematosus. Claimed TCR peptides (AAW11741-65) are
CC derived from the V(beta)5 family, or are functional derivatives of
CC V(beta)5 peptides

XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ERQR 7
| | | |
Db 7 ERQR 10

RESULT 8

AAW11750

ID AAW11750 standard; peptide; 11 AA.

XX

AC AAW11750;

XX

DT 04-NOV-1997 (first entry)

XX

DE T-cell receptor peptide V(beta)5.2 (49-59)FV.

XX

KW T-cell receptor; TCR; V(beta)5.2; multiple sclerosis;

KW rheumatoid arthritis; myasthenia gravis; encephalomyelitis; diabetes;

KW inflammatory bowel disease; systemic lupus erythematosus; thyroiditis;

KW therapy; diagnosis; vaccine.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 2

FT /note= "residue 2 is Tyr in V(beta)5.2 (49-59)F"

XX

PN WO9640778-A1.

XX

PD 19-DEC-1996.

XX

PF 06-JUN-1996; 96WO-US009423.

XX

PR 07-JUN-1995; 95US-00476405.

XX

PA (CONN-) CONNECTIVE THERAPEUTICS INC.

XX

PI Vandembark AA;

XX

DR WPI; 1997-099923/09.

XX

PT T cell receptor peptide derived from V(beta)-5 family - useful for
PT treating e.g. multiple sclerosis, myasthenia gravis, diabetes, etc.
XX
PS Claim 9; Page 42; 54pp; English.
XX
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CC of the V(beta)5.2 region (see AAW11767) of human T cell receptor (TCR).
CC It is a specifically preferred peptide for use in a claimed method for
CC the treatment, prevention or suppression of a T-cell mediated disease
CC such as multiple sclerosis, rheumatoid arthritis, myasthenia gravis,
CC encephalomyelitis, thyroiditis, diabetes, inflammatory bowel disease or
CC systemic lupus erythematosus. Claimed TCR peptides (AAW11741-65) are
CC derived from the V(beta)5 family, or are functional derivatives of
CC V(beta)5 peptides
XX
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ERQR 7
| | | |
Db 7 ERQR 10

RESULT 9
AAY31014

ID AAY31014 standard; peptide; 11 AA.
XX
AC AAY31014;
XX
DT 21-OCT-1999 (first entry)
XX
DE Non-crosslinked protein particle peptide 63.
XX
KW Non-crosslinked protein particle; diagnostic; therapy; monodisperse;
KW albumin; haemoglobin; nanometer; micrometer; clearance.
XX
OS Synthetic.
XX
PN US5945033-A.
XX
PD 31-AUG-1999.
XX
PF 12-NOV-1996; 96US-00747137.
XX
PR 15-JAN-1991; 91US-00641720.
PR 13-OCT-1992; 92US-00959560.
PR 01-JUN-1993; 93US-00069831.
PR 14-MAR-1994; 94US-00212546.
XX
PA (HEMO-) HEMOSPHERE INC.
XX
PI Yen RCK;
XX
DR WPI; 1999-508153/42.

XX
PT Non-crosslinked protein particles for therapeutic and diagnostic use.
XX
PS Example 22; Col 77-78; 65pp; English.
XX
CC This invention describes a novel aqueous suspension of monodisperse
CC particles on non-crosslinked, non-denatured albumin (50-5000 nm) which is
CC stable against dissolving upon dilution with an alcohol-free aqueous
CC medium. The method involves (a) forming an aqueous solution containing
CC albumin and hemoglobin and (b) treating the aqueous solution with an
CC alcohol to cause the solution to become turbid. The particles are useful
CC as agents for in vivo administration, either of their own administration
CC or as a vehicle for other therapeutic or diagnostic agents. The method
CC permits the formation of albumin and hemoglobin particles in the
CC nanometer and micrometer size range, in a form closer to their natural
CC form than the forms of the prior art. The particles therefore constitute
CC a more closely controlled agent for in vivo administration, with greater
CC ease of clearance from the body after their period of usefulness.
CC AAY30952-Y31135 represent peptides used in the method of the invention
XX
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQRK 8
| | | |
Db 3 RQRK 6

RESULT 10

AAY88545
ID AAY88545 standard; peptide; 11 AA.
XX
AC AAY88545;
XX
DT 07-AUG-2000 (first entry)
XX
DE NCAM Igl binding peptide #17.
XX
KW NCAM; neural cell adhesion molecule; Igl; immunoglobulin domain 1;
KW neurite outgrowth promoter; proliferation; nerve damage; sclerosis;
KW impaired myelination; stroke; Parkinson's disease; memory; schizophrenia;
KW Alzheimer's disease; diabetes mellitus; circadian clock; nephrosis;
KW treatment; prosthetic nerve guide; treatment; nervous system.
XX
OS Synthetic.
XX
PN WO200018801-A2.
XX
PD 06-APR-2000.
XX
PF 23-SEP-1999; 99WO-DK000500.
XX
PR 29-SEP-1998; 98DK-00001232.
PR 29-APR-1999; 99DK-00000592.

XX
PA (RONN/) RONN L C B.
PA (BOCK/) BOCK E.
PA (HOLM/) HOLM A.
PA (OLSE/) OLSEN M.
PA (OSTE/) OSTERGAARD S.
PA (JENS/) JENSEN P H.
PA (POUL/) POULSEN F M.
PA (SORO/) SOROKA V.
PA (RALE/) RALETS I.
PA (BERE/) BEREZIN V.
XX
PI Ronn LCB, Bock E, Holm A, Olsen M, Ostergaard S, Jensen PH;
PI Poulsen FM, Soroka V, Ralets I, Berezin V;
XX
DR WPI; 2000-293111/25.
XX
PT Compositions that bind neural cell adhesion molecules useful for treating
PT disorders of the nervous system and muscles e.g. Alzheimer's and
PT Parkinson's diseases.
XX
PS Example 4; Page 25; 119pp; English.
XX
CC Neural cell adhesion molecule (NCAM) is a cellular adhesion molecule.
CC NCAM is found in three forms, two of which are transmembrane forms, while
CC the third is attached via a lipid anchor to the cell membrane. All three
CC NCAM forms have an extracellular structure consisting five immunoglobulin
CC domains (Ig domains). The Ig domains are numbered 1 to 5 from the N-
CC terminal. The present sequence represents a peptide which binds to the
CC NCAM Ig1 domain. The peptide can be used in a compound which binds to
CC NCAM-Ig1/Ig2 domains, and is capable of stimulating or promoting neurite
CC outgrowth from NCAM presenting cells, and is also capable of promoting
CC the proliferation of NCAM presenting cells. The compound may be used in
CC the treatment of normal, degenerated or damaged NCAM presenting cells.
CC The compound may in particular be used to treat diseases of the central
CC and peripheral nervous systems such as post operative nerve damage,
CC traumatic nerve damage, impaired myelination of nerve fibres, conditions
CC resulting from a stroke, Parkinson's disease, Alzheimer's disease,
CC dementias, sclerosis, nerve degeneration associated with diabetes
CC mellitus, disorders affecting the circadian clock or neuro-muscular
CC transmission and schizophrenia. Conditions affecting the muscles may also
CC be treated with the compound, such as conditions associated with impaired
CC function of neuromuscular connections (e.g. genetic or traumatic shock or
CC traumatic atrophic muscle disorders). Conditions of the gonads, pancreas
CC (e.g. diabetes mellitus types I and II), kidney (e.g. nephrosis), heart,
CC liver and bowel may also be treated using the compound. The compound is
CC used in a prosthetic nerve guide, and also to stimulate the ability to
CC learn, and to stimulate the memory of a subject
XX
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKKE 4
| | | |

RESULT 11

ABP19679

ID ABP19679 standard; peptide; 11 AA.

XX

AC ABP19679;

XX

DT 11-SEP-2003 (revised)

DT 15-JUL-2002 (first entry)

XX

DE HIV B62 super motif vpu peptide #17.

XX

KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;

KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;

KW vaccine; HIV infection; immunisation; virucide.

XX

OS Human immunodeficiency virus 1.

XX

PN WO200124810-A1.

XX

PD 12-APR-2001.

XX

PF 05-OCT-2000; 2000WO-US027766.

XX

PR 05-OCT-1999; 99US-00412863.

XX

PA (EPIM-) EPIMMUNE INC.

XX

PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;

PI Baker DM, Celis E, Kubo RT, Grey HM;

XX

DR WPI; 2001-354887/37.

XX

PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1.

XX

PS Claim 32; Page 272; 448pp; English.

XX

CC The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABL25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
CC be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines. An
CC additional advantage of an group-based vaccine approach is the ability to
CC combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced

CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RQRK 8
| | | |
Db 3 RQRK 6

RESULT 12

ABP17507

ID ABP17507 standard; peptide; 11 AA.

XX

AC ABP17507;

XX

DT 11-SEP-2003 (revised)

DT 15-JUL-2002 (first entry)

XX

DE HIV B27 super motif rev peptide #18.

XX

KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;

KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;

KW vaccine; HIV infection; immunisation; virucide.

XX

OS Human immunodeficiency virus 1.

XX

PN WO200124810-A1.

XX

PD 12-APR-2001.

XX

PF 05-OCT-2000; 2000WO-US027766.

XX

PR 05-OCT-1999; 99US-00412863.

XX

PA (EPIM-) EPIMMUNE INC.

XX

PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;

PI Baker DM, Celis E, Kubo RT, Grey HM;

XX

DR WPI; 2001-354887/37.

XX

PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1.

XX

PS Claim 32; Page 227; 448pp; English.

XX

CC The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABL25347 to

CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
 CC be used for immunising subjects against HIV-1 infections. The use of
 CC group-based vaccines has several advantages over traditional vaccines,
 CC particularly when compared to the use of whole antigens in vaccine
 CC compositions. There is evidence that the immune response to whole
 CC antigens is directed largely toward variable regions of the antigen,
 CC allowing for immune escape due to mutations. The groups for inclusion in
 CC an group-based vaccine may be selected from conserved regions of viral or
 CC tumour-associated antigens, which therefore reduces the likelihood of
 CC escape mutants. Furthermore, immunosuppressive groups that may be present
 CC in whole antigens can be avoided with the use of group-based vaccines. An
 CC additional advantage of an group-based vaccine approach is the ability to
 CC combine selected groups (CTL and HTL), and further, to modify the
 CC composition of the groups, achieving, for example, enhanced
 CC immunogenicity. Accordingly, the immune response can be modulated, as
 CC appropriate, for the target disease. Similar engineering of the response
 CC is not possible with traditional approaches. ABP11501 to ABP25412
 CC represent peptide sequences used in the exemplification of the present
 CC invention. (Updated on 11-SEP-2003 to standardise OS field)

XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ERQR 7

||||

Db 6 ERQR 9

RESULT 13

ABP14260

ID ABP14260 standard; peptide; 11 AA.

XX

AC ABP14260;

XX

DT 11-SEP-2003 (revised)

DT 15-JUL-2002 (first entry)

XX

DE HIV A02 super motif vpu peptide #43.

XX

KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;

KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;

KW vaccine; HIV infection; immunisation; virucide.

XX

OS Human immunodeficiency virus 1.

XX

PN WO200124810-A1.

XX

PD 12-APR-2001.

XX

PF 05-OCT-2000; 2000WO-US027766.

XX

PR 05-OCT-1999; 99US-00412863.

XX

PA (EPIM-) EPIMMUNE INC.

XX
 PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kubo RT, Grey HM;
 XX
 DR WPI; 2001-354887/37.
 XX
 PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
 PT peptide groups, useful for vaccinating against HIV-1.
 XX
 PS Claim 32; Page 160; 448pp; English.
 XX
 CC The present invention describes a composition (I) comprising a prepared
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
 CC be used for immunising subjects against HIV-1 infections. The use of
 CC group-based vaccines has several advantages over traditional vaccines,
 CC particularly when compared to the use of whole antigens in vaccine
 CC compositions. There is evidence that the immune response to whole
 CC antigens is directed largely toward variable regions of the antigen,
 CC allowing for immune escape due to mutations. The groups for inclusion in
 CC an group-based vaccine may be selected from conserved regions of viral or
 CC tumour-associated antigens, which therefore reduces the likelihood of
 CC escape mutants. Furthermore, immunosuppressive groups that may be present
 CC in whole antigens can be avoided with the use of group-based vaccines. An
 CC additional advantage of an group-based vaccine approach is the ability to
 CC combine selected groups (CTL and HTL), and further, to modify the
 CC composition of the groups, achieving, for example, enhanced
 CC immunogenicity. Accordingly, the immune response can be modulated, as
 CC appropriate, for the target disease. Similar engineering of the response
 CC is not possible with traditional approaches. ABP11501 to ABP25412
 CC represent peptide sequences used in the exemplification of the present
 CC invention. (Updated on 11-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQRK 8
 ||||
 Db 3 RQRK 6

RESULT 14
 ABP16618
 ID ABP16618 standard; peptide; 11 AA.
 XX
 AC ABP16618;
 XX
 DT 11-SEP-2003 (revised)
 DT 15-JUL-2002 (first entry)
 XX
 DE HIV A24 super motif vpu peptide #33.
 XX
 KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;

KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;
KW vaccine; HIV infection; immunisation; virucide.
XX
OS Human immunodeficiency virus 1.
XX
PN WO200124810-A1.
XX
PD 12-APR-2001.
XX
PF 05-OCT-2000; 2000WO-US027766.
XX
PR 05-OCT-1999; 99US-00412863.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
XX
DR WPI; 2001-354887/37.
XX
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1.
XX
PS Claim 32; Page 208; 448pp; English.
XX
CC The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABL25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
CC be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines. An
CC additional advantage of an group-based vaccine approach is the ability to
CC combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQRK 8
| | | |
Db 3 RQRK 6

RESULT 15

ABP24378

ID ABP24378 standard; peptide; 11 AA.

XX

AC ABP24378;

XX

DT 11-SEP-2003 (revised)

DT 15-JUL-2002 (first entry)

XX

DE HIV A24 motif vpu peptide #9.

XX

KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;

KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;

KW vaccine; HIV infection; immunisation; virucide.

XX

OS Human immunodeficiency virus 1.

XX

PN WO200124810-A1.

XX

PD 12-APR-2001.

XX

PF 05-OCT-2000; 2000WO-US027766.

XX

PR 05-OCT-1999; 99US-00412863.

XX

PA (EPIM-) EPIMMUNE INC.

XX

PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;

PI Baker DM, Celis E, Kubo RT, Grey HM;

XX

DR WPI; 2001-354887/37.

XX

PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1.

XX

PS Claim 32; Page 368; 448pp; English.

XX

CC The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABL25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
CC be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
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CC tumour-associated antigens, which therefore reduces the likelihood of
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CC in whole antigens can be avoided with the use of group-based vaccines. An
CC additional advantage of an group-based vaccine approach is the ability to
CC combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as

CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RQRK 8
| | | |
Db 7 RQRK 10

RESULT 16

ABP14259

ID ABP14259 standard; peptide; 11 AA.

XX

AC ABP14259;

XX

DT 11-SEP-2003 (revised)

DT 15-JUL-2002 (first entry)

XX

DE HIV A02 super motif vpu peptide #42.

XX

KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;

KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;

KW vaccine; HIV infection; immunisation; virucide.

XX

OS Human immunodeficiency virus 1.

XX

PN WO200124810-A1.

XX

PD 12-APR-2001.

XX

PF 05-OCT-2000; 2000WO-US027766.

XX

PR 05-OCT-1999; 99US-00412863.

XX

PA (EPIM-) EPIMMUNE INC.

XX

PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;

PI Baker DM, Celis E, Kubo RT, Grey HM;

XX

DR WPI; 2001-354887/37.

XX

PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)

PT peptide groups, useful for vaccinating against HIV-1.

XX

PS Claim 32; Page 160; 448pp; English.

XX

CC The present invention describes a composition (I) comprising a prepared

CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid

CC sequence selected from 51 defined amino acid sequences (ABL25347 to

CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may

CC be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
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CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines. An
CC additional advantage of an group-based vaccine approach is the ability to
CC combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)

XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQRK 8

||||

Db 4 RQRK 7

RESULT 17

ABP16617

ID ABP16617 standard; peptide; 11 AA.

XX

AC ABP16617;

XX

DT 11-SEP-2003 (revised)

DT 15-JUL-2002 (first entry)

XX

DE HIV A24 super motif vpu peptide #32.

XX

KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;

KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;

KW vaccine; HIV infection; immunisation; virucide.

XX

OS Human immunodeficiency virus 1.

XX

PN WO200124810-A1.

XX

PD 12-APR-2001.

XX

PF 05-OCT-2000; 2000WO-US027766.

XX

PR 05-OCT-1999; 99US-00412863.

XX

PA (EPIM-) EPIMMUNE INC.

XX

PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kubo RT, Grey HM;
 XX
 DR WPI; 2001-354887/37.
 XX
 PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
 PT peptide groups, useful for vaccinating against HIV-1.
 XX
 PS Claim 32; Page 208; 448pp; English.
 XX
 CC The present invention describes a composition (I) comprising a prepared
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
 CC be used for immunising subjects against HIV-1 infections. The use of
 CC group-based vaccines has several advantages over traditional vaccines,
 CC particularly when compared to the use of whole antigens in vaccine
 CC compositions. There is evidence that the immune response to whole
 CC antigens is directed largely toward variable regions of the antigen,
 CC allowing for immune escape due to mutations. The groups for inclusion in
 CC an group-based vaccine may be selected from conserved regions of viral or
 CC tumour-associated antigens, which therefore reduces the likelihood of
 CC escape mutants. Furthermore, immunosuppressive groups that may be present
 CC in whole antigens can be avoided with the use of group-based vaccines. An
 CC additional advantage of an group-based vaccine approach is the ability to
 CC combine selected groups (CTL and HTL), and further, to modify the
 CC composition of the groups, achieving, for example, enhanced
 CC immunogenicity. Accordingly, the immune response can be modulated, as
 CC appropriate, for the target disease. Similar engineering of the response
 CC is not possible with traditional approaches. ABP11501 to ABP25412
 CC represent peptide sequences used in the exemplification of the present
 CC invention. (Updated on 11-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQRK 8
 ||||
 Db 4 RQRK 7

RESULT 18

ABP16616

ID ABP16616 standard; peptide; 11 AA.

XX

AC ABP16616;

XX

DT 11-SEP-2003 (revised)

DT 15-JUL-2002 (first entry)

XX

DE HIV A24 super motif vpu peptide #31.

XX

KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;

KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;

KW vaccine; HIV infection; immunisation; virucide.
 XX
 OS Human immunodeficiency virus 1.
 XX
 PN WO200124810-A1.
 XX
 PD 12-APR-2001.
 XX
 PF 05-OCT-2000; 2000WO-US027766.
 XX
 PR 05-OCT-1999; 99US-00412863.
 XX
 PA (EPIM-) EPIMMUNE INC.
 XX
 PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kubo RT, Grey HM;
 XX
 DR WPI; 2001-354887/37.
 XX
 PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
 PT peptide groups, useful for vaccinating against HIV-1.
 XX
 PS Claim 32; Page 208; 448pp; English.
 XX
 CC The present invention describes a composition (I) comprising a prepared
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
 CC be used for immunising subjects against HIV-1 infections. The use of
 CC group-based vaccines has several advantages over traditional vaccines,
 CC particularly when compared to the use of whole antigens in vaccine
 CC compositions. There is evidence that the immune response to whole
 CC antigens is directed largely toward variable regions of the antigen,
 CC allowing for immune escape due to mutations. The groups for inclusion in
 CC an group-based vaccine may be selected from conserved regions of viral or
 CC tumour-associated antigens, which therefore reduces the likelihood of
 CC escape mutants. Furthermore, immunosuppressive groups that may be present
 CC in whole antigens can be avoided with the use of group-based vaccines. An
 CC additional advantage of an group-based vaccine approach is the ability to
 CC combine selected groups (CTL and HTL), and further, to modify the
 CC composition of the groups, achieving, for example, enhanced
 CC immunogenicity. Accordingly, the immune response can be modulated, as
 CC appropriate, for the target disease. Similar engineering of the response
 CC is not possible with traditional approaches. ABP11501 to ABP25412
 CC represent peptide sequences used in the exemplification of the present
 CC invention. (Updated on 11-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQRK 8
 ||||
 Db 7 RQRK 10

RESULT 19

ABG69345

ID ABG69345 standard; peptide; 11 AA.

XX

AC ABG69345;

XX

DT 21-OCT-2002 (first entry)

XX

DE Human neural cell adhesion molecule (NCAM) peptide #17.

XX

KW Human; neural cell adhesion molecule; NCAM; heart muscle cell survival;

KW acute myocardial infarction; central nervous system disorder; stroke;

KW peripheral nervous system disorder; postoperative nerve damage;

KW traumatic nerve damage; spinal cord injury; nerve fibre; schizophrenia;

KW postischaemic damage; multiinfarct dementia; multiple sclerosis;

KW nerve degeneration; diabetes mellitus; neuro-muscular degeneration;

KW Alzheimer's disease; Parkinson's disease;

KW Huntington's disease. atrophic muscle disorder; gonad degeneration;

KW nephrosis.

XX

OS Homo sapiens.

XX

PN WO200247719-A2.

XX

PD 20-JUN-2002.

XX

PF 12-DEC-2001; 2001WO-DK000822.

XX

PR 12-DEC-2000; 2000DK-00001863.

XX

PA (ENKA-) ENKAM PHARM AS.

XX

PI Bock E, Berezin V, Kohler LB;

XX

DR WPI; 2002-583473/62.

XX

PT Use of a compound comprising a peptide of neural cell adhesion molecule,
PT in the preparation of medicament for preventing death of cells presenting
PT NCAM or NCAM ligand and treating central nervous system diseases.

XX

PS Disclosure; Page 16; 57pp; English.

XX

CC The invention relates to use of a compound (I) comprising a peptide which
CC comprises at least 5 contiguous amino acid residues of a sequence of the
CC neural cell adhesion molecule (NCAM), its fragment, variant or its mimic,
CC for the preparation of a medicament for preventing death of cells
CC presenting the NCAM or an NCAM ligand. (I) is useful in the preparation
CC of a medicament for preventing death of cells presenting the NCAM or an
CC NCAM ligand. The medicament is for the stimulation of the survival of
CC heart muscle cells, such as survival after acute myocardial infarction.
CC The medicament is for the treatment of diseases or conditions of the
CC central and peripheral nervous system, such as postoperative nerve
CC damage, traumatic nerve damage, e.g. resulting from spinal cord injury,
CC impaired myelination of nerve fibres, postischaemic damage, e.g.
CC resulting from a stroke, multiinfarct dementia, multiple sclerosis, nerve
CC degeneration associated with diabetes mellitus, neuro-muscular

CC degeneration, schizophrenia, Alzheimer's disease, Parkinson's disease and
CC Huntington's disease. The medicament is for the treatment of diseases or
CC conditions of the muscles including conditions with impaired function of
CC neuro-muscular connections, such as genetic or traumatic atrophic muscle
CC disorders, and for the treatment of diseases of conditions of various
CC organs, such as degenerative conditions of the gonads, pancreas (e.g.
CC diabetes mellitus type I and II) and kidney (e.g. nephrosis). ABG69329-
CC ABG69352 represent human NCAM peptides of the invention

XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKKE 4
||||
Db 1 AKKE 4

RESULT 20

AAO18039

ID AAO18039 standard; peptide; 11 AA.

XX

AC AAO18039;

XX

DT 30-AUG-2002 (first entry)

XX

DE Human immunoglobulin E epitope SEQ ID NO: 31.

XX

KW Allergy; immunoglobulin E; IgE; vaccine; immunogen; epitope; human;
KW non-anaphylactogenic; antiallergic.

XX

OS Homo sapiens.

XX

PN WO200234288-A2.

XX

PD 02-MAY-2002.

XX

PF 24-OCT-2001; 2001WO-EP012392.

XX

PR 27-OCT-2000; 2000GB-00026334.

XX

PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

XX

PI Vinals Y De BassolsC;

XX

DR WPI; 2002-479702/51.

XX

PT New peptides epitopes and mimotopes derived from IgE, useful for treating
PT or preventing allergies, for typing circulating anti-IgE, or for
PT diagnosing atopy.

XX

PS Claim 1; Page 5; 28pp; English.

XX

CC The present invention provides peptide epitopes derived from human
CC immunoglobulin E (IgE), which are non-anaphylactogenic and can be used as

CC immunogens to diagnose and treat allergies. The present sequence is an
CC epitope of the invention
XX
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ERQR 7
 ||||
Db 2 ERQR 5

RESULT 21

AAP60142

ID AAP60142 standard; peptide; 11 AA.

XX

AC AAP60142;

XX

DT 25-MAR-2003 (revised)

DT 31-OCT-2002 (revised)

DT 07-JUL-1991 (first entry)

XX

DE Type 3 pentapeptide linked to VP3 peptide suitable for use in a vaccine
DE against a disease caused by type 3 poliovirus.

XX

KW Vaccine; diagnosis; enterovirus disease; poliovirus type 1; type 2;
KW type 3.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Region 1. .5

FT /label= type 3 pentapeptide

FT Misc-difference 1

FT /label= R,K

FT /note= "pref. R"

FT Misc-difference 2

FT /label= N,Q,D,E

FT /note= "pref. N"

FT Misc-difference 3

FT /label= see above

FT Misc-difference 5

FT /label= D,E

FT /note= "pref. D"

FT Region 6. .11

FT /label= VP3 peptide

XX

PN EP197772-A.

XX

PD 15-OCT-1986.

XX

PF 03-APR-1986; 86EP-00302481.

XX

PR 03-APR-1985; 85GB-00008685.

PR 03-APR-1986; 86GB-00008140.

XX
PA (NATR) NAT RES DEV CORP.
PA (BRTE-) BRITISH TECHNOLOGY GROUP LTD.
XX
PI Minor PD, Evans DMA, Schild GC, Almond JW, Ferguson M;
XX
DR WPI; 1986-273645/42.
XX
PT Synthetic peptide for vaccination or diagnosis of enter-virus disease -
PT comprises fragment coded for by polio virus type 3 Sabin strain capsid
PT protein RNA.
XX
PS Disclosure; Page 15; 53pp; English.
XX
CC The inventors claim synthetic peptides for use in vaccination against or
CC diagnosis of a disease caused by an enterovirus (see AAN60118). The
CC peptides are coded for by codons 286-288 or 286-290 in the RNA sequence
CC coding for the structural capsid protein VP1 of poliovirus type 3 Sabin
CC strain or by equivalent codons of another enterovirus, or antigenic
CC equivs. Also claimed are synthetic peptides comprising the above peptides
CC linked to (a) a hexapeptide coded for by codons 93-98 as above, or (b) a
CC peptide sequence comprising AA residues 58 and 59 of the VP3 capsid
CC protein of an enterovirus. Typical doses are 100mg-1mg, i.m. (Updated on
CC 31-OCT-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct
CC PA field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KDT 10
| | |
Db 9 KDT 11

RESULT 22

AAP71164

ID AAP71164 standard; protein; 11 AA.

XX

AC AAP71164;

XX

DT 25-MAR-2003 (revised)

DT 03-OCT-2002 (revised)

DT 04-APR-1991 (first entry)

XX

DE Peptide which inhibits the binding of fibrinogen to platelets.

XX

KW Fibrinogen; platelets; cancer; cell attachment.

XX

OS Synthetic.

XX

PN EP220957-A.

XX

PD 06-MAY-1987.

XX

PF 27-OCT-1986; 86EP-00308335.
 XX
 PR 28-OCT-1985; 85US-00791872.
 XX
 PA (SCRI) SCRIPPS CLINIC & RES FOUND.
 XX
 PI Zimmerman TS, Ruggeri ZM, Houghten R;
 XX
 DR WPI; 1987-124477/18.
 XX
 PT New peptide(s) - useful for modulating cell adhesion and inhibiting
 PT binding of adhesive proteins to blood platelets esp. in treating cancers.
 XX
 PS Claim 19; Page 7; 7pp; English.
 XX
 CC The peptide inhibits the binding of fibrinogen to platelets and inhibits
 CC the aggregation of cells or platelets to each other since it modulates
 CC cell adhesion and inhibits the binding of adhesive proteins to blood
 CC platelets. The peptide has superior activity to known peptides and has
 CC similar properties. The peptide is useful for therapeutic and diagnostic
 CC purposes, esp. for inhibiting cell-cell attachment and cell growth
 CC phenomena such as cancer. (Updated on 03-OCT-2002 to add missing OS
 CC field.) (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RQR 7
 |||
 Db 6 RQR 8

RESULT 23
 AAP90643
 ID AAP90643 standard; protein; 11 AA.
 XX
 AC AAP90643;
 XX
 DT 10-MAR-2003 (revised)
 DT 09-AUG-1990 (first entry)
 XX
 DE Signal peptide NOS Synthetic.
 XX
 KW NOS; signal peptide; nucleolus.
 XX
 OS Unidentified.
 XX
 PN JP01096196-A.
 XX
 PD 14-APR-1989.
 XX
 PF 08-OCT-1987; 87JP-00252377.
 XX
 PR 08-OCT-1987; 87JP-00252377.

XX
 PA (HATA/) HATANAKA S.
 XX
 DR WPI; 1989-155085/21.
 XX
 PT New peptide NOS having specific aminoacid sequence - used to localise
 PT protein in nucleolus.
 XX
 PS Claim 1; Page 1; 12pp; Japanese.
 XX
 CC The peptide is useful for localising a protein in the nucleolus. DNA
 CC encoding it is inserted downstream of promoter in a plasmid to give pNOS
 CC Synthetic. DNA encoding an opt protein is also ligated into the vector,
 CC and the pNOS introduced to a host (eg E.coli). Plasmid DNA is then
 CC extracted from the cells and transfected into eukaryotic cells which have
 CC a nucleolus. Protein localisation can be detected immunologically within
 CC hours. See also AAP90642-4. (Updated on 10-MAR-2003 to add missing OS
 CC field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7
 |||
 Db 6 RQR 8

RESULT 24

AAR02183

ID AAR02183 standard; protein; 11 AA.

XX

AC AAR02183;

XX

DT 10-MAR-2003 (revised)

DT 02-AUG-1990 (first entry)

XX

DE Peptide which binds to Immunoglobulin E (IgE) receptors inhibiting IgE
 DE binding.

XX

KW Immunoglobulin E (IgE); anti-allergic drug; IgE binding inhibitor.

XX

OS Unidentified.

XX

FH Key Location/Qualifiers

FT Misc-difference 1

FT /label= OTHER

FT /note= "H-Ala"

FT Misc-difference 11

FT /label= OTHER

FT /note= "Phe-OH"

XX

PN JP01299298-A.

XX

PD 04-DEC-1989.

XX
 PF 27-MAY-1988; 88JP-00129721.
 XX
 PR 27-MAY-1988; 88JP-00129721.
 XX
 PA (KYOW) KYOWA HAKKO KOGYO KK.
 XX
 DR WPI; 1990-019330/03.
 XX
 PT Peptides which bind to IgE receptors inhibiting IgE binding - used as
 PT antiallergic drug having no side effects.
 XX
 PS Claim 2; Page 843; 8pp; Japanese.
 XX
 CC It is the new sequence No 15 and has an anti-allergic effect. It binds to
 CC IgE receptors on cell surfaces and inhibits IgE binding to receptors. It
 CC can be used as an anti-allergic drug, having no side effects. (Updated on
 CC 10-MAR-2003 to add missing OS field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QRK 8
 |||
 Db 7 QRK 9

RESULT 25

AAR06031

ID AAR06031 standard; protein; 11 AA.
 XX
 AC AAR06031;
 XX
 DT 25-MAR-2003 (revised)
 DT 20-NOV-1990 (first entry)
 XX
 DE Oligopeptide, antigenic to N.meningitidis.
 XX
 KW Meningococcal disease; meningitis; vaccine;
 KW Class I outer membrane protein; ds.
 XX
 OS Neisseria meningitidis.
 XX
 PN WO9006696-A.
 XX
 PD 28-JUN-1990.
 XX
 PF 19-DEC-1988; 88NL-00003111.
 XX
 PR 19-DEC-1988; 88NL-00003111.
 PR 06-JAN-1989; 89NL-00000036.
 PR 26-JUN-1989; 89NL-00001612.
 XX
 PA (PRAX-) PRAXIS BILOGICS IN.

PA (VOLK-) RIJKINSINST VOLKSGEZONDH.
 PA (SEID/) SEID R C.
 PA (NEVW-) NEDERLAND VERT MIN VAN.
 XX
 PI Seid RC, Paradiso PR, Poolman JT, Hoogerhout P, Wiertz EJ;
 PI Vanderley P, Heckels JE, Clarke IN;
 XX
 DR WPI; 1990-224326/29.
 XX
 PT Meningococcus class 1 outer-membrane protein vaccine - useful to immunise
 PT against meningococcal disease.
 XX
 PS Claim 50; Page 102; 120pp; English.
 XX
 CC Peptides derived from outer membrane, encoding homo/heterologous product
 CC such as a antigen-flagelin fusion protein, are useful in eliciting a
 CC strong and wide ranging immune response against most serotypes. (Updated
 CC on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KDT 10
 |||
 Db 3 KDT 5

RESULT 26

AAR08092

ID AAR08092 standard; protein; 11 AA.

XX

AC AAR08092;

XX

DT 25-MAR-2003 (revised)

DT 01-MAR-1991 (first entry)

XX

DE Antifreeze segment #2 encoded by SS3.

XX

KW synthetic antifreeze polypeptide; cryopreservation;

KW core repetitive sequence.

XX

OS Synthetic.

XX

PN WO9013571-A.

XX

PD 15-NOV-1990.

XX

PF 10-MAY-1989; 89US-00350481.

XX

PR 10-MAY-1989; 89US-00350481.

PR 10-APR-1990; 90US-00507716.

XX

PA (DNAP) DNA PLANT TECHN COR.

XX

PI Warren GJ, Mueller JM, Mckown RJ, Dunsmuir P;
 XX
 DR WPI; 1990-361428/48.
 XX
 PT New anti-freeze poly-peptide(s) - used for cryo-protection of e.g. foods,
 PT medically used biological(s), plant prods. or plants during growth.
 XX
 PS Disclosure; Fig 4; 11lpp; English.
 XX
 CC Synthetic anti-freeze polypeptides (saf) comprise a specifically
 CC cleavable site and a region containing at least two "core" segments such
 CC as the 11mer given here. The saf's suppress ice crystal growth by binding
 CC to the growing crystal face and blocking sites for further crystal
 CC growth. They can be used to maximise retention of important properties of
 CC organic materials through freezing and thawing processes. The basic
 CC design of the polypeptides is based on known antifreeze polypeptides from
 CC insects and fish, e.g. the winter flounder. See also AAQ06649-Q06652,
 CC AAQ06656, AAQ06658, AAQ06660-Q06672, AAR08070-6, AAR08087-R08091,
 CC AAR08093. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-
 CC MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PI
 CC field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
 |||
 Db 8 AKK 10

RESULT 27

AAR15673

ID AAR15673 standard; protein; 11 AA.

XX

AC AAR15673;

XX

DT 25-MAR-2003 (revised)

DT 13-FEB-1992 (first entry)

XX

DE Asn-residue specific protease Asn-component.

XX

KW Asparagine; Asn; protease; transpeptidation; amine; DNP.

XX

OS Synthetic.

XX

PN EP458475-A.

XX

PD 27-NOV-1991.

XX

PF 30-APR-1991; 91EP-00303884.

XX

PR 21-MAY-1990; 90JP-00129148.

XX

PA (TAKI) TAKARA SHUZO CO LTD.

XX
 PI Koyama N, Kato I, Matsushita H, Abe Y, Ishii SI;
 XX
 DR WPI; 1991-348154/48.
 XX
 PT Asparagine-residue specific protease - used as trans:peptisation reagent
 PT for the prepn. of peptide(s) esp. physiologically active peptide(s).
 XX
 PS Disclosure; Page 7; 12pp; English.
 XX
 CC This peptide is used as Asn component and GG, GGH, G-NH2 or GG-NH2 as the
 CC amine component. The reaction was carried out at 37 deg C for 3 hrs. with
 CC the pH 7.7. The reaction mix. was analysed by C18 reversed-phase HPLC.
 CC The transpeptidation prod. is shown in AAR15674. See also AAR15672-74.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7
 |||
 Db 8 RQR 10

RESULT 28

AAR12168

ID AAR12168 standard; protein; 11 AA.

XX

AC AAR12168;

XX

DT 20-AUG-1991 (first entry)

XX

DE Neuropeptide Y analogue #3.

XX

KW neuropeptide Y; NPY; antagonist.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 2

FT /label= OTHER

FT /note= "8-aminooctanoic acid"

XX

PN DE3939797-A.

XX

PD 06-JUN-1991.

XX

PF 01-DEC-1989; 89DE-03939797.

XX

PR 01-DEC-1989; 89DE-03939797.

XX

PA (BADI) BASF AG.

XX

PI Zechel JC, Schult S, Unger L;

XX
 DR WPI; 1991-172223/24.
 XX
 PT New peptide(s) derived from neuro-peptide Y - are neuro-peptide Y
 PT antagonists, useful as hypotensives and in treatment of e.g. vessel
 PT spasms.
 XX
 PS Example 5; Page 5; 7pp; German.
 XX
 CC This peptide is a competitive antagonist of neuropeptide Y so is useful
 CC for treating high blood pressure and vascular spasms. It can also be used
 CC as a diagnostic/analytical reagent, e.g. for investigating biochemical or
 CC patho-physiological properties of neuropeptide Y. See also AAR12164,
 CC AAR12166-7 and AAR12169-R12175
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7
 |||
 Db 8 RQR 10

RESULT 29

AAR12171

ID AAR12171 standard; protein; 11 AA.

XX

AC AAR12171;

XX

DT 20-AUG-1991 (first entry)

XX

DE Neuropeptide Y analogue #6.

XX

KW neuropeptide Y; NPY; antagonist.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 3

FT /label= OTHER

FT /note= "8-aminooctanoic acid"

XX

PN DE3939797-A.

XX

PD 06-JUN-1991.

XX

PF 01-DEC-1989; 89DE-03939797.

XX

PR 01-DEC-1989; 89DE-03939797.

XX

PA (BADI) BASF AG.

XX

PI Zechel JC, Schult S, Unger L;

XX

DR WPI; 1991-172223/24.
 XX
 PT New peptide(s) derived from neuro-peptide Y - are neuro-peptide Y
 PT antagonists, useful as hypotensives and in treatment of e.g. vessel
 PT spasms.
 XX
 PS Example 27; Page 6; 7pp; German.
 XX
 CC This peptide is a competitive antagonist of neuropeptide Y so is useful
 CC for treating high blood pressure and vascular spasms. It can also be used
 CC as a diagnostic/analytical reagent, e.g. for investigating biochemical or
 CC patho-physiological properties of neuropeptide Y. See also AAR12164,
 CC AAR12166-R12170 and AAR12172-5
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7
 |||
 Db 8 RQR 10

RESULT 30

AAR12173

ID AAR12173 standard; protein; 11 AA.

XX

AC AAR12173;

XX

DT 20-AUG-1991 (first entry)

XX

DE Neuropeptide Y analogue #8.

XX

KW neuropeptide Y; NPY; antagonist.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /label= p-hydroxyphenylpropionyl-Pro

FT Misc-difference 2

FT /label= OTHER

FT /note= "8-aminooctanoic acid"

XX

PN DE3939797-A.

XX

PD 06-JUN-1991.

XX

PF 01-DEC-1989; 89DE-03939797.

XX

PR 01-DEC-1989; 89DE-03939797.

XX

PA (BADI) BASF AG.

XX

PI Zechel JC, Schult S, Unger L;

XX
 DR WPI; 1991-172223/24.
 XX
 PT New peptide(s) derived from neuro-peptide Y - are neuro-peptide Y
 PT antagonists, useful as hypotensives and in treatment of e.g. vessel
 PT spasms.
 XX
 PS Example 18; Page 6; 7pp; German.
 XX
 CC This peptide is a competitive antagonist of neuropeptide Y so is useful
 CC for treating high blood pressure and vascular spasms. It can also be used
 CC as a diagnostic/analytical reagent, e.g. for investigating biochemical or
 CC patho-physiological properties of neuropeptide Y. See also AAR12164,
 CC AAR12166-R12172 and AAR12174-5
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7
 |||
 Db 8 RQR 10

RESULT 31
 AAR22743

ID AAR22743 standard; protein; 11 AA.
 XX
 AC AAR22743;
 XX
 DT 25-MAR-2003 (revised)
 DT 27-AUG-1992 (first entry)
 XX
 DE Non-A, Non-B hepatitis virus antibody binding peptide.
 XX
 KW NANBH; immunoreactive; detection.
 XX
 OS Synthetic.
 XX
 PN EP479376-A.
 XX
 PD 08-APR-1992.
 XX
 PF 05-OCT-1990; 90EP-00202658.
 XX
 PR 26-SEP-1991; 91EP-00202498.
 XX
 PA (ALKU) AKZO NV.
 XX
 PI Habets WJA;
 XX
 DR WPI; 1992-116131/15.
 XX
 PT New peptide(s) reactive with antibodies to hepatitis non-A, non-B, virus
 PT - for detection of NANBH and its antibodies in body fluids.

XX
PS Example; Page 7; 9pp; English.
XX
CC The sequence is that of a peptide which is immunoreactive with antibodies
CC to hepatitis non-A, non-B (NANBH) virus, it was prepd. by stepwise solid
CC phase peptide synthesis. It can be used to detect NANBH antibodies in
CC test fluids. It has improved immunochemical reactivity, a high affinity
CC to NANBH antibodies and is of a safe, non-infectious origin. See also
CC AAR22727-R22744. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QRK 8
| | |
Db 1 QRK 3

RESULT 32

AAR35381

ID AAR35381 standard; peptide; 11 AA.

XX

AC AAR35381;

XX

DT 25-MAR-2003 (revised)

DT 07-JUN-1993 (first entry)

XX

DE Amphiphilic peptide #112 used to treat oral infections.

XX

KW Adverse oral conditions; amphipathic; anti-bacterial; anti-viral;

KW anti-fungal; dental plaque; dental caries; periodontal disease;

KW gingivitis; ionophore; ion-channel forming.

XX

OS Synthetic.

XX

PN WO9301723-A1.

XX

PD 04-FEB-1993.

XX

PF 09-JUL-1992; 92WO-US005757.

XX

PR 25-JUL-1991; 91US-00735070.

XX

PA (MAGA-) MAGAININ PHARM INC.

XX

PI Berkowitz B, Jacob L;

XX

DR WPI; 1993-058434/07.

XX

PT Peptide(s) for prophylaxis and treatment of oral disorders - used for
PT periodontal disease, plaque, dental caries, gingivitis, etc.

XX

PS Claim 2; Page 129; 143pp; English.

XX

CC This is a specific example of a highly generic formula covering preferred
CC amphiphilic peptides for use in preventing or treating adverse oral
CC conditions. The peptide is an ionophore (i.e. an ion- channel forming
CC peptide) which has anti-bacterial, anti-viral, anti- fungal activity,
CC etc. making it suitable for use in oral compositions to treat or prevent
CC periodontal disease, plaque, dental caries, halitosis and gingivitis. The
CC anti-bacterial action will also be useful against bacteria associated
CC with dental implant infections and the peptides can stimulate the healing
CC of wounds in the oral cavity. (Updated on 25-MAR-2003 to correct PN
CC field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3

|||

Db 1 AKK 3

RESULT 33

AAR32351

ID AAR32351 standard; peptide; 11 AA.

XX

AC AAR32351;

XX

DT 05-JUL-1993 (first entry)

XX

DE Human Factor X peptide.

XX

KW Anticoagulant; intrinsic; extrinsic; prothrombin activation; thrombin;
KW formation; Factor Xa; pathway mediated activation; inhibition.

XX

OS Synthetic.

XX

PN US5187155-A.

XX

PD 16-FEB-1993.

XX

PF 23-JUN-1989; 89US-00371561.

XX

PR 23-JUN-1989; 89US-00371561.

XX

PA (TEXA) UNIV TEXAS SYSTEM.

XX

PI Fair DS;

XX

DR WPI; 1993-075751/09.

XX

PT Compsns. comprising peptide(s) of 10-50 aminoacid residues - inhibit
PT factor X activation and/or Factor Xa function, useful for preventing
PT blood clot formation and treating deep vein thrombosis, pulmonary
PT embolism, etc.

XX

PS Example; Page 6; 23pp; English.

XX
CC The sequence is that of a peptide corresponding to amino acids 384-394 of
CC the human factor X molecule which was tested for its effect, (as a % of
CC the control rate), on the rate of Factor Xa formation and on the rate of
CC thrombin formation. The results obtd. were for activation of Factor X by
CC the extrinsic activation complex 100%, by the intrinsic activation
CC complex 72%, and activation by RVV-X, 85%. For the rate of thrombin
CC formation the rate was 100% as compared to the control rate

XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KDT 10
|||
Db 5 KDT 7

RESULT 34

AAR33973

ID AAR33973 standard; peptide; 11 AA.

XX

AC AAR33973;

XX

DT 25-MAR-2003 (revised)

DT 21-JUL-1993 (first entry)

XX

DE Amphiphilic peptide (e), #2.

XX

KW Hydrophobic; hydrophilic; neutral; (e); ionophore; channel-forming;

KW human; virus; antimicrobial; antiviral; antibacterial; antitumour;

KW antiparasitic; spermicide; preservative; sterilant; disinfectant;

KW wound healing; burn; infection; eye; cysts; spores; trophozoites; plants;

KW contamination.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "May be acetylated"

FT Modified-site 11

FT /note= "May be amidated"

XX

PN WO9305802-A1.

XX

PD 01-APR-1993.

XX

PF 04-SEP-1992; 92WO-US007622.

XX

PR 13-SEP-1991; 91US-00760054.

PR 20-APR-1992; 92US-00870960.

XX

PA (MAGA-) MAGAININ PHARM INC.

XX

PI Maloy WL, Kari UP, Williams JI;

XX
 DR WPI; 1993-117245/14.
 XX
 PT New biologically active amphiphilic peptide cpds. - having ion channel-
 PT forming properties used for inhibiting growth of target cells, virus or
 PT viral-infected cells.
 XX
 PS Claim 27; Page 33; 46pp; English.
 XX
 CC This sequence is an example of a biologically active peptide which
 CC corresponds to the generic sequence; R1-R2-R2-R1-R1-R2-R1-R2-R2-R1
 CC where R1 = a hydrophobic amino acid; and R2 = a basic hydrophilic or
 CC neutral hydrophilic amino acid. This basic structure was designated (e).
 CC Peptides such as this are ionophores ie. they have channel-forming
 CC properties. The peptides can be administered to a host, eg, humans, to
 CC inhibit the growth of a target cell, virus or virally infected cell. They
 CC can be used as antimicrobial, antiviral agents, antibacterial agents,
 CC antitumour agents, antiparasitic agents, and as spermicides. They can be
 CC used as preservatives or sterilants or disinfectants. These peptides can
 CC also be used to promote or stimulate healing of wounds, to treat and/or
 CC prevent prevent skin or burn infections, to prevent or treat eye
 CC infections and to kill cysts, spores or trophozoites of infection causing
 CC organisms. The peptides may also be administered to plants to prevent or
 CC treat microbial, viral or parasitic contamination. (Updated on 25-MAR-
 CC 2003 to correct PN field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
 |||
 Db 1 AKK 3

RESULT 35

AAR31163

ID AAR31163 standard; peptide; 11 AA.

XX

AC AAR31163;

XX

DT 25-MAR-2003 (revised)

DT 10-MAY-1993 (first entry)

XX

DE C-terminal substd. amphiphilic peptide #112.

XX

KW ion-channel forming; ionophore; antibiotic; anti-tumour; anti-virus;

KW wound healing.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 11

FT /note= "Leu-(C=O)-T, T= O-R, NH-NH2, NH-OH or NR'R''; R=

FT opt.substd. 1-10C aliphatic, aromatic or aralkyl gp.; R',

FT R''= H or from one of gps. i and ii; gp.i= 1-10C hydroxy-
 FT substd. aliphatic, aromatic or aralkyl gp.; gp.ii= amino-
 FT substd. aliphatic, aromatic, aralkyl or alkylaromatic gp.
 FT and at least one of R' and R'' = gp.i or gp.ii'''
 XX
 PN WO9222317-A1.
 XX
 PD 23-DEC-1992.
 XX
 PF 01-JUN-1992; 92WO-US004603.
 XX
 PR 12-JUN-1991; 91US-00713716.
 XX
 PA (MAGA-) MAGAININ PHARM INC.
 XX
 PI Maloy WL, Kari UP;
 XX
 DR WPI; 1993-017904/02.
 XX
 PT New C-terminal-substd. amphiphilic peptide(s) - for treating bacterial,
 PT viral or fungal infections and tumours, also useful as spermicide.
 XX
 PS Claim 21; Page 114; 124pp; English.
 XX
 CC This peptide is a preferred example of a highly generic amphiphilic
 CC peptide with a C-terminal modification which increases the peptide's
 CC biological activity c.f. the unmodified peptide. The preferred C-terminal
 CC modification is -(CO)-NHCH2CH2OH or -(CO)-NHCH2CH2NH2. Such substd.
 CC peptides may be used for inhibiting the growth of a target cell, virus or
 CC virally-infected cell in a host. The peptides have a broad range of
 CC potent antibiotic activity, e.g. against gram- negative and gram-positive
 CC bacteria, fungi, protozoa and parasites. The peptides can also be used to
 CC promote wound healing and treatment of burns. Other preferred amphiphilic
 CC peptides include magainins and their analogues, PGLa, XPF, CPF, a
 CC cecropin and a sarcotoxin. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
 |||
 Db 1 AKK 3

RESULT 36

AAR34248

ID AAR34248 standard; peptide; 11 AA.

XX

AC AAR34248;

XX

DT 25-MAR-2003 (revised)

DT 04-AUG-1993 (first entry)

XX

DE Mutant HTLV-I residues 88-98, peptide 2L-1.2.

XX
 KW Human T-cell leukaemia virus; hydrophilic; conjugate; aggregate;
 KW diagnosis; antibodies; gp46; mutant; gag; T cell epitope.
 XX
 OS Synthetic.
 XX
 PN WO9306843-A1.
 XX
 PD 15-APR-1993.
 XX
 PF 08-OCT-1992; 92WO-US008405.
 XX
 PR 08-OCT-1991; 91US-00771553.
 XX
 PA (UYDU-) UNIV DUKE.
 XX
 PI Palker TJ, Haynes BF;
 XX
 DR WPI; 1993-134125/16.
 XX
 PT Antigenic determinant peptide(s) of HTLV envelope glyco:protein - useful
 PT for detecting anti-HTLV-I and -II antibodies and as vaccine against HTLV.
 XX
 PS Example 7; Page 32; 50pp; English.
 XX
 CC To determine which amino acids within the HTLV-I envelope amino acids 88-
 CC 98 were required for absorption of neutralising anti-peptide antibodies
 CC to HTLV-I, 11 peptides (2L1.1-2L1.11) were synthesised in which
 CC sequential amino acids were each replaced by the amino acid alanine.
 CC These 11 mutated peptides, as well as peptide 2L-1 bearing the native
 CC HTLV-I sequence were tested and identified that amino acids 90, 92, 93
 CC and 95 were important for HTLV-I neutralisation. See also AAR34225-57.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
 |||
 Db 2 AKK 4

RESULT 37

AAR30442

ID AAR30442 standard; peptide; 11 AA.

XX

AC AAR30442;

XX

DT 25-MAR-2003 (revised)

DT 17-MAY-1993 (first entry)

XX

DE Synthetic sequence of glycoalbumin immunogen.

XX

KW V8; trypsin; glycosylation; albumin; glucose; diabetes.

XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 7
 FT /note= "in vivo glycosylated"
 XX
 PN US5173422-A.
 XX
 PD 22-DEC-1992.
 XX
 PF 03-MAY-1990; 90US-00518681.
 XX
 PR 22-AUG-1986; 86US-00899456.
 PR 02-JUN-1987; 87US-00054131.
 PR 19-FEB-1988; 88US-00158200.
 XX
 PA (MILE) MILES INC.
 XX
 PI Knowles WJ, Marchesi VT;
 XX
 DR WPI; 1993-017567/02.
 XX
 PT Monoclonal antibody specific for human glyco-albumin - used for determ.
 PT of extent of glycosylation of albumin in monitoring glucose level in
 PT diabetes.
 XX
 PS Disclosure; Page 14; 22pp; English.
 XX
 CC The sequence shows a preferred synthetic glycosylated peptide from
 CC glycoalbumin. The peptide can be linked to a conventional immunogenic
 CC carrier material to form an immunogen. The immunogen may be used to raise
 CC monoclonal antibodies which are useful for the detection of the
 CC glycosylated form of albumin in human blood samples. This serves as a
 CC useful index of glucose level control in diabetics. See also AAR30460-71,
 CC AAR30439-47, AAR30478-9, and AAR31165-78. (Updated on 25-MAR-2003 to
 CC correct PF field.) (Updated on 25-MAR-2003 to correct PR field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ERQ 6
 |||
 Db 2 ERQ 4

RESULT 38
 AAR30463
 ID AAR30463 standard; peptide; 11 AA.
 XX
 AC AAR30463;
 XX
 DT 25-MAR-2003 (revised)
 DT 17-MAY-1993 (first entry)

XX
DE Synthetic sequence of glycoalbumin in the region of lysine 525.
XX
KW V8; trypsin; glycosylation; albumin; glucose; diabetes.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 7
FT /note= "corresponds to lysine 525 and is in vivo
FT glycosylated"
XX
PN US5173422-A.
XX
PD 22-DEC-1992.
XX
PF 03-MAY-1990; 90US-00518681.
XX
PR 22-AUG-1986; 86US-00899456.
PR 02-JUN-1987; 87US-00054131.
PR 19-FEB-1988; 88US-00158200.
XX
PA (MILE) MILES INC.
XX
PI Knowles WJ, Marchesi VT;
XX
DR WPI; 1993-017567/02.
XX
PT Monoclonal antibody specific for human glyco-albumin - used for determ.
PT of extent of glycosylation of albumin in monitoring glucose level in
PT diabetes.
XX
PS Disclosure; Fig 1; 22pp; English.
XX
CC The sequence shows a preferred synthetic glycosylated peptide from
CC glycoalbumin in the region of lysine 525. The peptide can be linked to a
CC conventional immunogenic carrier material to form an immunogen. The
CC immunogen may be used to raise monoclonal antibodies which are useful for
CC the detection of the glycosylated form of albumin in human blood samples.
CC This serves as a useful index of glucose level control in diabetics. See
CC also AAR30460-71, AAR30439-47, AAR30478-9, and AAR31165-78. (Updated on
CC 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PR
CC field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ERQ 6
|||
Db 2 ERQ 4

RESULT 39
AAR30478

ID AAR30478 standard; peptide; 11 AA.
 XX
 AC AAR30478;
 XX
 DT 25-MAR-2003 (revised)
 DT 17-MAY-1993 (first entry)
 XX
 DE Synthetic sequence of glycoalbumin immunogen.
 XX
 KW V8; trypsin; glycosylation; albumin; glucose; diabetes.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 7
 FT /note= "in vivo glycosylated"
 XX
 PN US5173422-A.
 XX
 PD 22-DEC-1992.
 XX
 PF 03-MAY-1990; 90US-00518681.
 XX
 PR 22-AUG-1986; 86US-00899456.
 PR 02-JUN-1987; 87US-00054131.
 PR 19-FEB-1988; 88US-00158200.
 XX
 PA (MILE) MILES INC.
 XX
 PI Knowles WJ, Marchesi VT;
 XX
 DR WPI; 1993-017567/02.
 XX
 PT Monoclonal antibody specific for human glyco-albumin - used for determ.
 PT of extent of glycosylation of albumin in monitoring glucose level in
 PT diabetes.
 XX
 PS Disclosure; Page 12; 22pp; English.
 XX
 CC The sequence shows a preferred synthetic glycosylated peptide from
 CC glycoalbumin. The peptide can be linked to a conventional immunogenic
 CC carrier material to form an immunogen. The immunogen may be used to raise
 CC monoclonal antibodies which are useful for the detection of the
 CC glycosylated form of albumin in human blood samples. This serves as a
 CC useful index of glucose level control in diabetics. See also AAR30460-71,
 CC AAR30439-47, AAR30479, and AAR31165-78. (Updated on 25-MAR-2003 to
 CC correct PF field.) (Updated on 25-MAR-2003 to correct PR field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ERQ 6
 |||
 Db 2 ERQ 4

RESULT 40

AAR41495

ID AAR41495 standard; peptide; 11 AA.

XX

AC AAR41495;

XX

DT 23-FEB-1994 (first entry)

XX

DE TNF inhibitory peptide VII.

XX

KW Tumour necrosis factor; TNF; inhibition; solid phase synthesis; ss.

XX

OS Synthetic.

XX

PN JP05194594-A.

XX

PD 03-AUG-1993.

XX

PF 21-JAN-1992; 92JP-00029044.

XX

PR 21-JAN-1992; 92JP-00029044.

XX

PA (SAGA) SAGAMI CHEM RES CENTRE.

XX

DR WPI; 1993-282916/36.

XX

PT TNF inhibitory novel peptide(s) - include N-terminal amino Gp. which is
PT opt. modified with acetyl, T-butoxy-carbonyl or benzyl-oxy-carbonyl Gp.
PT and C-terminal carboxy Gp. is opt. amidated.

XX

PS Claim 1; Page 6; 8pp; Japanese.

XX

CC The sequences given in AAR41489-99 are tumour necrosis factor (TNF)
CC inhibitory peptides. They may optionally be modified at the N- terminal
CC with an acetyl, t-butoxycarbonyl or benzyloxycarbonyl, and at the C-
CC terminal they are optionally amidated. These peptides are produced by
CC solid phase synthesis methods and may be produced at low cost

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3

|||

Db 3 AKK 5

RESULT 41

AAR39369

ID AAR39369 standard; peptide; 11 AA.

XX

AC AAR39369;

XX

DT 25-MAR-2003 (revised)
 DT 07-DEC-1993 (first entry)
 XX
 DE Human glycoalbumin peptide ALB C11L.
 XX
 KW glycosylated albumin; immunogen; diabetes; diagnosis;
 KW monoclonal antibody.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1
 FT /note= "enables specific coupling of the peptide to
 FT immunogenic carrier"
 FT Modified-site 6
 FT /note= "potential site of further glycosylation during
 FT synthesis"
 FT Modified-site 7
 FT /note= "glycosylated Lys525"
 XX
 PN US5225354-A.
 XX
 PD 06-JUL-1993.
 XX
 PF 21-AUG-1992; 92US-00934085.
 XX
 PR 22-AUG-1986; 86US-00899456.
 PR 02-JUN-1987; 87US-00054131.
 PR 19-FEB-1988; 88US-00158200.
 PR 03-MAY-1990; 90US-00518681.
 XX
 PA (MOLE-) MOLECULAR DIAGNOSTICS INC.
 XX
 PI Knowles WJ, Marchesi VT;
 XX
 DR WPI; 1993-226613/28.
 XX
 PT Immunoassay for glycosylated albumin in blood - using monoclonal antibody
 PT which binds specifically to human albumin glycosylated at lysine residue
 PT 525.
 XX
 PS Claim 10; Fig 1; 22pp; English.
 XX
 CC Novel monoclonal antibodies are specific for glycosylated human albumin
 CC in the region around Lys(525). Antibodies are pref. raised against
 CC peptides having the sequence Lys(519)-Glu(531), or their N- and/or C-
 CC terminal deletions, provided Lys(525) is present. Additional Tyr and/or
 CC Cys residues are opt. present at one or both peptide termini. The
 CC determination of the extent of glycosylation of albumin in an
 CC individual's blood provides a useful index of glucose level control in
 CC diabetics. (Updated on 25-MAR-2003 to correct PF field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ERQ 6
 | | |
Db 2 ERQ 4

RESULT 42

AAR45132

ID AAR45132 standard; peptide; 11 AA.

XX

AC AAR45132;

XX

DT 25-MAR-2003 (revised)

DT 28-JUN-1994 (first entry)

XX

DE Amphiphilic peptide for N-terminal lipophilic substitution.

XX

KW Ion channel; magainin; PGLa; XPF; CPF; cecropin; sarcotoxin; amphiphilic;

KW hydrophobic; hydrophilic; lipophilic; growth; inhibition; target cell;

KW virus; virally-infected cell; antimicrobial; antiviral; antitumour;

KW antiparasitic; spermicide; wound healing; burn; infection.

XX

OS Synthetic.

XX

PN WO9324138-A1.

XX

PD 09-DEC-1993.

XX

PF 27-MAY-1993; 93WO-US005192.

XX

PR 01-JUN-1992; 92US-00891201.

XX

PA (MAGA-) MAGAININ PHARM INC.

XX

PI Kari U;

XX

DR WPI; 1993-405419/50.

XX

PT Peptide(s) or proteins with an N-terminal lipophilic substit. - used for

PT inhibiting growth of target cell, virus or virally-infected cell.

XX

PS Disclosure; Page 97-103; 113pp; English.

XX

CC A novel compsn. for inhibiting growth of a target cell, virus or virally-

CC infected cell comprises a peptide of formula T-N(W)-X (I). X is a

CC biologically active amphiphilic ion channel-forming peptide or protein;

CC pref. a magainin peptide, a PGLa peptide, a XPF peptide, a CPF peptide, a

CC cecropin or a sarcotoxin. N is the nitrogen of the N-terminal amino

CC group. T is a lipophilic moiety; pref. R-CO, where R is a 2-16C

CC hydrocarbon (alkyl or aromatic or alkylaromatic). T is pref. an octanoyl

CC group. W is T or hydrogen. Amphiphilic peptides as examples of X are

CC given in AAR45115-138. The N-terminal substd. peptides and proteins have

CC increased biological activity as compared with unsubstd. peptides or

CC proteins or peptides substd. at the N-terminal with an acetyl gp. They

CC can be used as antimicrobial agents, antiviral agents, antitumour agents,

CC antiparasitic agents or spermicides and can also exhibit other bioactive

CC functions. They can also be used in promoting or stimulating wound

CC healing, for the treatment of external burns and to treat and/or prevent
CC skin and burn infections or eye infections. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
|||
Db 1 AKK 3

RESULT 43

AAR34421

ID AAR34421 standard; peptide; 11 AA.

XX

AC AAR34421;

XX

DT 25-MAR-2003 (revised)

DT 05-AUG-1993 (first entry)

XX

DE Hepatitis C Ab detection peptide #5.

XX

KW Test reagent; detection; antibody; hepatitis C; virus; HCV; epitope;

KW structural region; diagnosis; ss.

XX

OS Synthetic.

XX

PN WO9307488-A1.

XX

PD 15-APR-1993.

XX

PF 02-OCT-1992; 92WO-JP001276.

XX

PR 02-OCT-1991; 91JP-00255524.

PR 26-MAR-1992; 92JP-00068695.

XX

PA (EIKE) EIKEN KAGAKU KK.

PA (OSAU) UNIV OSAKA.

PA (TANA) TANABE SEIYAKU CO.

XX

PI Ishibashi K, Ito M, Yoshida I, Takamizawa A, Shibatani T;

XX

DR WPI; 1993-134624/16.

XX

PT Reagent for detecting antibodies to hepatitis C virus - comprises

PT peptide(s) with the same sequence as an epitope of an HCV structural

PT region.

XX

PS Disclosure; Page 43; 51pp; Japanese.

XX

CC The sequences given in AAR34417-25 are peptides which can be used in a

CC test reagent for the detection of antibodies against hepatitis C. The

CC peptides represent epitopes of an HCV structural region and they react

CC specifically with antibodies against the HCV structural region. Detection
CC is sensitive and accurate and allows diagnosis of the infection at a
CC very early stage. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QRK 8
|||
Db 1 QRK 3

RESULT 44

AAR55163

ID AAR55163 standard; protein; 11 AA.

XX

AC AAR55163;

XX

DT 25-MAR-2003 (revised)

DT 11-JAN-1995 (first entry)

XX

DE Fragment of retinoic acid receptor RAR-beta.

XX

KW Liver; hap; retinoic acid receptor; steroid; thyroid; hormone; hepatoma;
KW retinoid; antibody.

XX

OS Homo sapiens.

XX

PN US5317090-A.

XX

PD 31-MAY-1994.

XX

PF 11-DEC-1992; 92US-00989902.

XX

PR 16-DEC-1987; 87US-00133687.

PR 17-DEC-1987; 87US-00134130.

PR 20-JUN-1988; 88US-00209009.

PR 30-NOV-1988; 88US-00278136.

PR 30-MAR-1989; 89US-00330405.

PR 21-AUG-1991; 91US-00751612.

PR 30-MAR-1992; 92US-00860577.

XX

PA (INSP) INST PASTEUR.

XX

PI Marchio A, Chambon P, Petkovich M, Krust A, Dejean A, Tiollais P;
PI Brand N, De The HB;

XX

DR WPI; 1994-176333/21.

XX

PT Antibody specific for retinoic acid receptor-beta - useful for detecting,
PT quantifying and identifying agonists and antagonists of retinoid
PT activity.

XX

PS Claim 4; Col 40; 35pp; English.

XX
CC The retinoic acid receptor RAR-beta is encoded by a gene designated hap.
CC The hap gene is transcribed at low level in most human tissues, but the
CC gene is overexpressed in prosate and kidney. Six out of seven hepatoma or
CC hepatoma-derived cell lines express a small hap transcript which is
CC undetectable in normal adult and foetal livers but present in all non-
CC hepatic tissues tested. (Updated on 25-MAR-2003 to correct PF field.)

XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKE 4
|||
Db 7 KKE 9

RESULT 45

AAR50563

ID AAR50563 standard; peptide; 11 AA.

XX

AC AAR50563;

XX

DT 25-MAR-2003 (revised)

DT 18-OCT-1994 (first entry)

XX

DE Amphiphilic peptide #112.

XX

KW Amphiphilic; ion forming; gynaecological malignancy; magainin; PGLa; XPF;

KW CPF; cecropin; sarcotoxin; melittin; apidaecin; defensin;

KW major basic protein; eosinophils; uterine; cervical; cancer;

KW bacterial permeability increasing protein; ovarian; stage IC.

XX

OS Synthetic.

XX

PN WO9405313-A1.

XX

PD 17-MAR-1994.

XX

PF 16-AUG-1993; 93WO-US007798.

XX

PR 31-AUG-1992; 92US-00937462.

XX

PA (MAGA-) MAGAININ PHARM INC.

XX

PI Jacob LS, Maloy WL, Baker MA;

XX

DR WPI; 1994-100851/12.

XX

PT Treating gynaecological tumours with amphiphilic peptide(s) - which form
PT ion channels, e.g. magainin or PGLa peptide(s), partic. for treating
PT ovarian, uterine or cervical cancers.

XX

PS Disclosure; Page 116; 130pp; English.

XX

CC The sequences given in AAR50452-568 represent amphiphilic, ion forming
CC peptides which may be used to treat gynaecological malignancy. These
CC peptides are based on magainin, PGLa, XPF or CPF, a cecropin, a
CC sarcotoxin, melittin, an apidaecin, a defensin, major basic protein of
CC eosinophils or a bacterial permeability increasing protein. These
CC peptides are esp. used to treat ovarian, esp. stage IC, uterine or
CC cervical cancers. (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 9.8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3

|||

Db 1 AKK 3

RESULT 46

AAR55987

ID AAR55987 standard; peptide; 11 AA.

XX

AC AAR55987;

XX

DT 25-MAR-2003 (revised)

DT 19-DEC-1994 (first entry)

XX

DE Ion channel forming peptide.

XX

KW Ion channel forming peptide; tumour; skin disease; malignancy; melanoma;

KW carcinoma; basal cell; squamous cell; magainin; PGLa; CPF peptides;

KW cecropins; sarcotoxin; melittin; apidocin; defensins;

KW major basic protein; bacteria-permeability increasing protein; perforin.

XX

OS Synthetic.

XX

PN WO9412206-A1.

XX

PD 09-JUN-1994.

XX

PF 03-DEC-1993; 93WO-US011885.

XX

PR 03-DEC-1992; 92US-00984957.

XX

PA (MAGA-) MAGAININ PHARM INC.

XX

PI Jacob LS, Maloy WL;

XX

DR WPI; 1994-199965/24.

XX

PT Treating skin cancer with ion channel forming peptide(s) - e.g.

PT magainins, melittin etc., specifically for treating melanoma.

XX

PS Disclosure; Page 121; 136pp; English.

XX

CC The peptide is used to treat dermatological malignancies. It may be used

CC to treat especially melanoma but also basal cell and squamous cell
CC carcinomas. It can be used together with an ion which also
CC inhibits/prevents growth of the target cell. Peptides used for such
CC therapy include magainin, PGLa or CPF peptides; cercopins, sarcotoxins,
CC mellitin, apidocins, defensins, major basic protein of eosinophils;
CC bacteria-permeability increasing protein and perforin. See also AAQ55876-
CC Q55997. (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
|||
Db 1 AKK 3

RESULT 47

AAR59065

ID AAR59065 standard; peptide; 11 AA.

XX

AC AAR59065;

XX

DT 25-MAR-2003 (revised)

DT 21-APR-1995 (first entry)

XX

DE Cancer treating, amphiphilic ion-channel forming peptide.

XX

KW Amphiphilic ion-channel forming peptide; cancer treatment;
KW protease inhibitors.

XX

OS Synthetic.

XX

PN WO9419369-A1.

XX

PD 01-SEP-1994.

XX

PF 22-FEB-1994; 94WO-US002121.

XX

PR 26-FEB-1993; 93US-00021607.

XX

PA (MAGA-) MAGAININ PHARM INC.

XX

PI Herlyn M, Jacob LS, Maloy WL;

XX

DR WPI; 1994-294258/36.

XX

PT Treating cancerous growths - by administering biologically active
PT peptide(s) and protease inhibitors.

XX

PS Claim 2; Page 106; 124pp; English.

XX

CC AAR59060 to AAR59066 are a group of amphiphilic ion-channel forming
CC peptides conforming to the same generic sequence. Used in combination
CC with one or more protease inhibitors and other amphiphilic ion-channel

CC forming peptides or proteins; they are effective in the treatment of
CC cancerous growths. In particular during surgery and radiation treatment
CC they may be useful in inhibiting, preventing and/or destroying potential
CC "loose" malignant cells capable of colonising other sites. (Updated on 25
CC -MAR-2003 to correct PN field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
|||
Db 1 AKK 3

RESULT 48

AAR56948

ID AAR56948 standard; peptide; 11 AA.

XX

AC AAR56948;

XX

DT 25-MAR-2003 (revised)

DT 17-MAR-1995 (first entry)

XX

DE Peptide which neutralises bacterial endotoxin.

XX

KW septic shock; bacterial endotoxin; lipopolysaccharide; LPS;

KW gram negative bacteria; conjugate moiety; septicemia; neutralising;

KW longer activity; polyvinylpyrrolidone; dextran; hetastarch;

KW polyvinyl alcohol; ion-channel forming; amphiphilic.

XX

OS Synthetic.

XX

PN WO9413697-A1.

XX

PD 23-JUN-1994.

XX

PF 06-DEC-1993; 93WO-US011841.

XX

PR 07-DEC-1992; 92US-00987443.

XX

PA (MAGA-) MAGAININ PHARM INC.

XX

PI Hendi M, Rao M, Williams TJ;

XX

DR WPI; 1994-217804/26.

XX

PT New conjugates of bioactive amphiphilic peptide(s) and conjugate moiety -
PT are useful for treatment of septic shock.

XX

PS Disclosure; Page 115; 141pp; English.

XX

CC Septic shock is often due to the body's reaction to foreign

CC lipopolysaccharide (LPS). The compounds of the invention neutralise

CC bacterial endotoxins without neutralising essential proteins in the

CC plasma of patients, eg.heparins. They also have longer duration of
CC activity than unconjugated peptides. In general peptides such as this are
CC ion-channel forming peptides.The compounds are biologically active
CC peptides linked to a conjugate moiety, eg. carbohydrates, proteins,
CC polyvinylpyrrolidone, polyalkylene glycols and polyvinyl alcohols. The
CC conjugate moiety may be linked at the C- or N-terminal or internally of
CC the peptide. AAR55591-631 and AAR56879-957 are examples of these peptide-
CC conjugate moiety compounds (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3

|||

Db 1 AKK 3

RESULT 49

AAR50448

ID AAR50448 standard; peptide; 11 AA.

XX

AC AAR50448;

XX

DT 25-MAR-2003 (revised)

DT 17-OCT-1994 (first entry)

XX

DE Amphiphilic peptide #113.

XX

KW Amphiphilic peptide; aprotic organic solvent; alcohol; antitumour;

KW antibiotic; antimicrobial; antifungal; antiparasitic; anticancer;

KW antiviral; human; animal; plant; ion-channel; forming peptide.

XX

OS Synthetic.

XX

PN WO9405308-A1.

XX

PD 17-MAR-1994.

XX

PF 13-AUG-1993; 93WO-US007694.

XX

PR 28-AUG-1992; 92US-00936504.

XX

PA (MAGA-) MAGAININ PHARM INC.

XX

PI Williams JI;

XX

DR WPI; 1994-100846/12.

XX

PT Purifying amphiphilic protein or peptide by solvent extn. - partic. for
PT recombinant, ion-channel forming peptide(s) such as magainins, avoids use
PT of chaotropic agents.

XX

PS Disclosure; Page 124; 135pp; English.

XX

CC The sequences given in AAR50336-451 are amphiphilic peptides which were
CC isolated by the method of the invention. A material containing
CC amphiphilic peptides such as these, was treated with a mixt. of aprotic
CC organic solvent and alcohol to form a single miscible solution. This
CC solution was then treated with a aqueous solution to form an aqueous
CC phase solution containing the peptides and an organic solvent phase, and
CC the peptides were isolated from the aqueous phase. The isolated peptides
CC may be useful as antibiotic, antimicrobial, antifungal, antiparasitic,
CC antitumour, anticancer, and/or antiviral agents for treatment of humans,
CC animals or plants. These peptides are esp. ion-channel forming peptides
CC which enable biologically active ions to enter cells. (Updated on 25-MAR-
CC 2003 to correct PN field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3

|||

Db 1 AKK 3

RESULT 50

AAR51276

ID AAR51276 standard; protein; 11 AA.

XX

AC AAR51276;

XX

DT 25-MAR-2003 (revised)

DT 09-SEP-1994 (first entry)

XX

DE Meningococcal OMP Pl.16 epitope.

XX

KW Neisseria meningitidis; meningococcus; outer membrane protein; OMP;

KW outer membrane vesicle; lipopolysaccharide; vaccine.

XX

OS Synthetic.

XX

PN W09408021-A1.

XX

PD 14-APR-1994.

XX

PF 30-JUL-1993; 93WO-NL000163.

XX

PR 02-OCT-1992; 92NL-00001716.

XX

PA (NEWE-) NEDERLANDEN MIN WELZIJN.

XX

PI Van Der Ley PA, Poolman JT, Hoogerhout P;

XX

DR WPI; 1994-135585/16.

DR N-PSDB; AAQ62053.

XX

PT New B cell activating molecules from meningococcal lipo:polysaccharide -

PT and derived peptide conjugates, outer membrane vesicles etc. useful in

PT vaccines effective against several meningococcal immunotypes.
 XX
 PS Example; Page 25; 62pp; English.
 XX
 CC An oligonucleotide with KpnI sticky ends (AAQ62053) encodes the P1.16
 CC epitope of Neisseria meningitidis outer membrane protein (OMP). The 3'
 CC end of the antisense strand overhangs the 5' end of the sense strand by 4
 CC bases, and the 3' end of the sense strand overhangs the 5' end of the
 CC antisense strand by 4 bases. Eptiopes encoded by the sense and antisense
 CC strands are given in AAR51276 and AAR55835, respectively. The
 CC oligonucleotide was placed in loop 6 of the class I OMP gene, providing a
 CC new meningococcal strain with an extra epitope for use in vaccines.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KDT 10
 |||
 Db 3 KDT 5

RESULT 51

AAR51277

ID AAR51277 standard; protein; 11 AA.

XX

AC AAR51277;

XX

DT 25-MAR-2003 (revised)

DT 09-SEP-1994 (first entry)

XX

DE Meningococcal OMP P1.16 epitope.

XX

KW Neisseria meningitidis; meningococcus; outer membrane protein; OMP;

KW outer membrane vesicle; lipopolysaccharide; vaccine.

XX

OS Synthetic.

XX

PN WO9408021-A1.

XX

PD 14-APR-1994.

XX

PF 30-JUL-1993; 93WO-NL000163.

XX

PR 02-OCT-1992; 92NL-00001716.

XX

PA (NEWE-) NEDERLANDEN MIN WELZIJN.

XX

PI Van Der Ley PA, Poolman JT, Hoogerhout P;

XX

DR WPI; 1994-135585/16.

DR N-PSDB; AAQ62054.

XX

PT New B cell activating molecules from meningococcal lipo:polysaccharide -

PT and derived peptide conjugates, outer membrane vesicles etc. useful in
PT vaccines effective against several meningococcal immunotypes.
XX
PS Example; Page 26; 62pp; English.
XX
CC An oligonucleotide with SpeI sticky ends (AAQ62054) encodes the P1.16
CC epitope of Neisseria meningitidis outer membrane protein (OMP). The 3'
CC end of the antisense strand overhangs the 5' end of the sense strand by 4
CC bases, and the 3' end of the sense strand overhangs the 5' end of the
CC antisense strand by 4 bases. Eptiopes encoded by the sense and antisense
CC strands are given in AAR51277 and AAR55836, respectively. The
CC oligonucleotide was placed in loop 5 of the class I OMP gene, providing a
CC new meningococcal strain with an extra epitope for use in vaccines.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KDT 10
|||
Db 3 KDT 5

RESULT 52

AAR82678

ID AAR82678 standard; protein; 11 AA.
XX
AC AAR82678;
XX
DT 23-JAN-1996 (first entry)
XX
DE V8 fragment of CD45 associating protein pp32.
XX
KW CD45; immune system; disease; pp32; T-lymphocyte; T-cell; activation;
KW isoform; CD2; phorbol ester; identification; screening;
KW monoclonal antibody.
XX
OS Homo sapiens.
XX
PN W09521916-A2.
XX
PD 17-AUG-1995.
XX
PF 09-FEB-1995; 95WO-US001618.
XX
PR 14-FEB-1994; 94US-00197793.
XX
PA (BADI) BASF AG.
XX
PI Schoenhaut D, Ratnofsky S, Meuer S, Schraven B;
XX
DR WPI; 1995-293118/38.
DR N-PSDB; AAT03910.
XX

PT Nucleic acid encoding a human pp32 protein which associates with CD45 -
PT useful for treatment of immune system diseases and in the identification
PT of T cell activation inhibitors.

XX

PS Example 9; Page 25; 49pp; English.

XX

CC pp32 is specifically associated with, and is a potential substrate of
CC CD45. pp32 is constitutively phosphorylated on serine in resting T-
CC cells. In such cells it exists in two isoforms, pp32 low and pp32 high.
CC Both isoforms show rapid changes during T-cell activation. These changes
CC take place within five minutes after stimulation of T- lymphocytes with
CC monoclonal antibodies specific for CD2 or with Phorbol esters. pp32 is
CC useful for treating diseases of the immune system and to identify
CC inhibitors of T-cell activation. Peptide fragments of pp32 (AAR82673-81)
CC were used to produce degenerate primers (AAT03911-19) which were then
CC used to produce a probe to isolate a full length pp32 cDNA clone

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ERQ 6

|||

Db 9 ERQ 11

RESULT 53

AAW21496

ID AAW21496 standard; peptide; 11 AA.

XX

AC AAW21496;

XX

DT 16-OCT-2003 (revised)

DT 30-JUL-1997 (first entry)

XX

DE Hepatitis delta antigen derived signal oligopeptide #1.

XX

KW Hydrophilic; signal oligopeptide; hydrophilicity maxima; vaccine; SIV;
KW competitive inhibitor; feedback regulator; synthesis; gastrin precursor;
KW charge; polarity; farnesyl synthetase; plasminogen activator inhibitor 1;
KW hydroxymethylglutaryl coenzyme A reductase; glucagon precursor; rhesus;
KW gonadoliberin precursor; plasminogen activator inhibitor 2; prorenin;
KW Alzheimer amyloid A4; corticotropin releasing factor binding protein;
KW apolipoprotein E; herpes virus 1 glycoprotein B; HSV1; human; OMVVS;
KW herpes virus 2 glycoprotein B; HSV2; collagenase; apolipoprotein A;
KW Treponema pallidum membrane protein; TMPA; islet amyloid polypeptide;
KW fibroblast MMP1; schistosoma elastase precursor; schistosomin;
KW hepatitis delta antigen; rev protein; HIV; VILV; angiotensinogen.

XX

OS Hepatitis D virus.

XX

PN W09519568-A1.

XX

PD 20-JUL-1995.

XX

PF 12-JAN-1995; 95WO-US000575.

XX

PR 14-JAN-1994; 94US-00182248.

XX

PA (RATH/) RATH M.

XX

PI Rath M;

XX

DR WPI; 1995-263953/34.

XX

PT Identifying signal oligopeptide(s) in protein sequence(s) - shown as
PT regions of max. hydrophilicity, used in modulating communication between
PT protein(s).

XX

PS Claim 5; Page 72; 88pp; English.

XX

CC The sequences given in AAW21201-560 represent hydrophilic signal oligo-
CC peptides. These signal oligopeptides are localised on the surface of the
CC protein and are represented by the hydrophilicity maxima of the protein.
CC These peptides are enriched in charged amino acids arranged with neutral
CC spacer amino acids. The specific signal character of these oligopeptides
CC is determined by a characteristic combination of conformation and charge
CC within the signal sequence. These oligopeptides may be used as vaccines
CC in the treatment of human disease, as competitive inhibitors to prevent
CC or reduce the metabolic action or interaction of a selected protein by
CC blocking its specific signal sequences, or as therapeutic agents to
CC function as feedback regulators to reduce synthesis rate of a selected
CC protein. These peptides may be modified by omitting one or more amino
CC acids at the N- and/or C-terminal, by substituting one or more amino
CC acids without consideration of charge and polarity, by substituting one
CC or more amino acids with amino acid residues with similar charge and/or
CC polarity, by omitting one or more amino acids or a combination of these.
CC (Updated on 16-OCT-2003 to standardise OS field)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 9.8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RKD 9

|||

Db 3 RKD 5

RESULT 54

AAW21220

ID AAW21220 standard; peptide; 11 AA.

XX

AC AAW21220;

XX

DT 29-JUL-1997 (first entry)

XX

DE Farnesyl synthetase derived signal oligopeptide #20.

XX

KW Hydrophilic; signal oligopeptide; hydrophilicity maxima; vaccine; SIV;

KW competitive inhibitor; feedback regulator; synthesis; gastrin precursor;

KW charge; polarity; farnesyl synthetase; plasminogen activator inhibitor 1;
KW hydroxymethylglutaryl coenzyme A reductase; glucagon precursor; rhesus;
KW gonadoliberin precursor; plasminogen activator inhibitor 2; prorenin;
KW Alzheimer amyloid A4; corticotropin releasing factor binding protein;
KW apolipoprotein E; herpes virus 1 glycoprotein B; HSV1; human; OMVVS;
KW herpes virus 2 glycoprotein B; HSV2; collagenase; apolipoprotein A;
KW Treponema pallidum membrane protein; TMPA; islet amyloid polypeptide;
KW fibroblast MMP1; schistosoma elastase precursor; schistosomin;
KW hepatitis delta antigen; rev protein; HIV; VILV; angiotensinogen.

XX

OS Homo sapiens.

XX

PN W09519568-A1.

XX

PD 20-JUL-1995.

XX

PF 12-JAN-1995; 95WO-US000575.

XX

PR 14-JAN-1994; 94US-00182248.

XX

PA (RATH/) RATH M.

XX

PI Rath M;

XX

DR WPI; 1995-263953/34.

XX

PT Identifying signal oligopeptide(s) in protein sequence(s) - shown as
PT regions of max. hydrophilicity, used in modulating communication between
PT protein(s).

XX

PS Claim 5; Page 26; 88pp; English.

XX

CC The sequences given in AAW21201-560 represent hydrophilic signal oligo-
CC peptides. These signal oligopeptides are localised on the surface of the
CC protein and are represented by the hydrophilicity maxima of the protein.
CC These peptides are enriched in charged amino acids arranged with neutral
CC spacer amino acids. The specific signal character of these oligopeptides
CC is determined by a characteristic combination of conformation and charge
CC within the signal sequence. These oligopeptides may be used as vaccines
CC in the treatment of human disease, as competitive inhibitors to prevent
CC or reduce the metabolic action or interaction of a selected protein by
CC blocking its specific signal sequences, or as therapeutic agents to
CC function as feedback regulators to reduce synthesis rate of a selected
CC protein. These peptides may be modified by omitting one or more amino
CC acids at the N- and/or C-terminal, by substituting one or more amino
CC acids without consideration of charge and polarity, by substituting one
CC or more amino acids with amino acid residues with similar charge and/or
CC polarity, by omitting one or more amino acids or a combination of these

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 9.8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3

|||

RESULT 55

AAR76917

ID AAR76917 standard; peptide; 11 AA.

XX

AC AAR76917;

XX

DT 08-MAR-1996 (first entry)

XX

DE Thymosin alpha-1 peptide analogue #23.

XX

KW Thymosin alpha-1; analogue; immune system modulator; alpha-interferon;
KW gamma-interferon; macrophage migration inhibitory factor; T-cell marker;
KW interleukin-2 receptor; helper T-cell; solid phase synthesis;
KW immunodeficiency; therapy; AIDS; HIV; immunodepravation.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 11

FT /note= "optionally amidated Pro or amidated Gly"

XX

PN WO9520602-A2.

XX

PD 03-AUG-1995.

XX

PF 18-JAN-1995; 95WO-US000617.

XX

PR 28-JAN-1994; 94US-00188232.

XX

PA (ALPH-) ALPHA 1 BIOMEDICALS INC.

XX

PI Wang S;

XX

DR WPI; 1995-275412/36.

XX

PT New thymosin alpha-1 peptide analogues - for the treatment of
PT immunodeficiency diseases and the reconstitution of immune functions in
PT immuno-depressed patients.

XX

PS Claim 7; Page ?; 24pp; English.

XX

CC The sequences represented by AAR76895-R76935 are thymosin alpha-1
CC analogues. Thymosin alpha-1 is an immune system modulator. Thymosin alpha
CC -1 activity includes, stimulation of alpha- and gamma-interferon
CC production, increasing macrophage migration inhibitory factor production,
CC inducing expression of T-cell markers (including interleukin-2
CC receptors), and improving helper T-cell activity. These sequences
CC function like natural thymosin alpha-1, and are easy to produce. These
CC sequences were synthesised by solid phase synthesis on a 4-
CC methylbenzhydrylamine resin. The peptides were cleaved from this resin
CC using trifluoromethane sulfonic acid (TFS). These sequences can be used
CC to reconstitute immune functions in immunodeprived and immunodepressed
CC patients. They can also be used in the treatment of immunodeficiency
CC diseases

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKE 4

|||

Db 1 KKE 3

RESULT 56

AAR84537

ID AAR84537 standard; peptide; 11 AA.

XX

AC AAR84537;

XX

DT 06-JUN-1996 (first entry)

XX

DE Hepatitis C virus core antigen (amino acids 8-18).

XX

KW Tailor-made; antigen/antibody specificity exchanger; HIV infection;

KW heavy chain; complementarity determining region; CDR;

KW human immunodeficiency virus; variable loop 3 domain; redirecting;

KW epitope; HCV; hepatitis C virus; core protein.

XX

OS Synthetic.

XX

PN WO9529938-A1.

XX

PD 09-NOV-1995.

XX

PF 27-APR-1995; 95WO-SE000468.

XX

PR 28-APR-1994; 94SE-00001460.

XX

PA (FERR) FERRING AB.

XX

PI Saellberg M;

XX

DR WPI; 1995-393040/50.

XX

PT Antigen-antibody specificity exchanger - used in a method to redirect a

PT patients antibodies against polio:virus to fight HIV infection in the

PT patient.

XX

PS Claim 7; Page 35; 38pp; English.

XX

CC An antigen/antibody specificity exchanger comprises an antibody- derived

CC amino acid sequence (A) which specifically binds to a particular antigen,

CC linked to an amino acid sequence (C) to which a particular antibody

CC binds. The present sequence is a preferred example of a type (C) sequence

CC ; it is an epitope from hepatitis C virus. Preferred type (A) sequences

CC are complementarity determining regions from e.g. anti-HIV-1 antibodies.

CC The specificity exchanger can redirect antibodies already present in a

CC patient and raised against a particular antigen, to fight a different

CC antigen. For example, it was shown that anti-poliovirus antibodies could
CC be redirected to fight HIV

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QRK 8

|||

Db 1 QRK 3

RESULT 57

AAR90259

ID AAR90259 standard; peptide; 11 AA.

XX

AC AAR90259;

XX

DT 10-JUL-1996 (first entry)

XX

DE Ion-channel forming peptide #111 with lipophilic N-terminal group.

XX

KW Ion channel forming peptide; lipophilic; N-terminal modification;

KW magainin; inhibition; cell growth; viral replication; ionophore;

KW membrane permeability; antimicrobial; anti-bacterial; antibiotic;

KW anti-fungal; anti-viral; spermicidal; anti-tumour; anti-parasitic.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "N-terminal amino group is mono- or di-substd. by

FT lipophilic moiety, esp. octanoyl"

XX

PN WO9519370-A1.

XX

PD 20-JUL-1995.

XX

PF 18-JAN-1995; 95WO-US000714.

XX

PR 18-JAN-1994; 94US-00184462.

XX

PA (MAGA-) MAGAININ PHARM INC.

XX

PI Kari U, Williams TJ, Mclane M;

XX

DR WPI; 1995-263826/34.

XX

PT Ion channel-forming amphiphilic peptide(s) with N-terminal lipophilic

PT gps. - useful e.g. as antiviral, antibacterial, antiparasitic or

PT antitumour agents.

XX

PS Claim 25; Page 108; 139pp; English.

XX

CC The present peptide is a specific example corresp. to a highly generic

CC formula for ion channel forming peptides (ionophores). These ionophores
 CC are known to have a broad range of potent antibiotic activity against
 CC microorganisms including gram-positive and gram-negative bacteria, fungi,
 CC viruses, protozoa and parasites. N-terminal modification (pref. mono-
 CC substn. by octanoyl) to produce an ion-channel forming peptide having a
 CC lipophilic N-terminus increases the biological activity of the peptides
 CC against target cells, viruses and virally-infected cells, compared to
 CC peptides substd. with an acetyl group at the N-terminus. Compositions
 CC comprising the peptides with lipophilic modifications are claimed for
 CC inhibiting growth of a target cell, virus or virally-infected cell
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
 |||
 Db 1 AKK 3

RESULT 58

AAR91788

ID AAR91788 standard; peptide; 11 AA.

XX

AC AAR91788;

XX

DT 11-JUL-1996 (first entry)

XX

DE Ion-channel forming peptide #123 with lipophilic N-terminal group.

XX

KW Ion channel forming peptide; lipophilic; N-terminal modification;
 KW magainin; inhibition; cell growth; viral replication; ionophore;
 KW membrane permeability; antimicrobial; anti-bacterial; antibiotic;
 KW anti-fungal; anti-viral; spermicidal; anti-tumour; anti-parasitic.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "N-terminal amino group is mono-substd. by
 FT octanoyl"

FT Modified-site 11

FT /note= "C-terminal amide"

XX

PN WO9519370-A1.

XX

PD 20-JUL-1995.

XX

PF 18-JAN-1995; 95WO-US000714.

XX

PR 18-JAN-1994; 94US-00184462.

XX

PA (MAGA-) MAGAININ PHARM INC.

XX

PI Kari U, Williams TJ, Mclane M;

XX
 DR WPI; 1995-263826/34.
 XX
 PT Ion channel-forming amphiphilic peptide(s) with N-terminal lipophilic
 PT gps. - useful e.g. as antiviral, antibacterial, antiparasitic or
 PT antitumour agents.
 XX
 PS Example 1; Page 111; 139pp; English.
 XX
 CC Various ion channel forming peptides (ionophores) in C-terminal amide
 CC form were modified by N-terminal substn. with a lipophilic group and then
 CC tested for activity against S.aureus ATCC 25923 (S), P.aeruginosa ATCC
 CC 27853 (P), E.coli ATCC 25922 (E) and C.albicans (C). Results indicated
 CC that when a biologically active peptide is substd. with a lipophilic
 CC moiety, the peptide has increased activity against a range of
 CC microorganisms. Compositions comprising such peptides with lipophilic
 CC modifications are claimed for inhibiting growth of a target cell, virus
 CC or virally-infected cell. Minimum inhibitory concentrations (in
 CC microgram/ml) for the present peptide against S, P, E and C,
 CC respectively, were: 32, 16, 32 and 32
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
 |||
 Db 7 AKK 9

RESULT 59

AAR91787

ID AAR91787 standard; peptide; 11 AA.

XX

AC AAR91787;

XX

DT 11-JUL-1996 (first entry)

XX

DE Ion-channel forming peptide #122 with lipophilic N-terminal group.

XX

KW Ion channel forming peptide; lipophilic; N-terminal modification;
 KW magainin; inhibition; cell growth; viral replication; ionophore;
 KW membrane permeability; antimicrobial; anti-bacterial; antibiotic;
 KW anti-fungal; anti-viral; spermicidal; anti-tumour; anti-parasitic.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "N-terminal amino group is mono-substd. by
 octanoyl"

FT Modified-site 11

FT /note= "C-terminal amide"

XX

PN W09519370-A1.

XX
 PD 20-JUL-1995.
 XX
 PF 18-JAN-1995; 95WO-US000714.
 XX
 PR 18-JAN-1994; 94US-00184462.
 XX
 PA (MAGA-) MAGAININ PHARM INC.
 XX
 PI Kari U, Williams TJ, Mclane M;
 XX
 DR WPI; 1995-263826/34.
 XX
 PT Ion channel-forming amphiphilic peptide(s) with N-terminal lipophilic
 PT gps. - useful e.g. as antiviral, antibacterial, antiparasitic or
 PT antitumour agents.
 XX
 PS Example 1; Page 111; 139pp; English.
 XX
 CC Various ion channel forming peptides (ionophores) in C-terminal amide
 CC form were modified by N-terminal substn. with a lipophilic group and then
 CC tested for activity against S.aureus ATCC 25923 (S), P.aeruginosa ATCC
 CC 27853 (P), E.coli ATCC 25922 (E) and C.albicans (C). Results indicated
 CC that when a biologically active peptide is substd. with a lipophilic
 CC moiety, the peptide has increased activity against a range of
 CC microorganisms. Compositions comprising such peptides with lipophilic
 CC modifications are claimed for inhibiting growth of a target cell, virus
 CC or virally-infected cell. Minimum inhibitory concentrations (in
 CC microgram/ml) for the present peptide against S, P, E and C,
 CC respectively, were: 32, 32, 64 and 64
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
 |||
 Db 7 AKK 9

RESULT 60
 AAR87902
 ID AAR87902 standard; peptide; 11 AA.
 XX
 AC AAR87902;
 XX
 DT 28-FEB-1996 (first entry)
 XX
 DE Neuropeptide Y agonist peptide.
 XX
 KW neuropeptide Y; NPY; agonist; hypertensive; vasoconstrictor;
 KW colon relaxing; gastric emptying diminution; eating disorder;
 KW anorexia nervosa.
 XX
 OS Synthetic.

XX
 FH Key Location/Qualifiers
 FT Modified-site 2
 FT /label= OTHER
 FT /note= "8-amino-octanoic acid residue"
 FT Modified-site 11
 FT /note= "Tyr-NH2"
 XX
 PN US5395823-A.
 XX
 PD 07-MAR-1995.
 XX
 PF 15-MAR-1993; 93US-00032526.
 XX
 PR 26-AUG-1988; 88US-00237591.
 PR 24-JUL-1989; 89US-00384373.
 PR 21-DEC-1990; 90US-00631755.
 PR 18-OCT-1991; 91US-00782890.
 PR 05-AUG-1992; 92US-00925546.
 XX
 PA (RICH) MERRELL DOW PHARM INC.
 XX
 PI Krstenansky JL;
 XX
 DR WPI; 1995-114851/15.
 XX
 PT New peptide agonists of neuropeptide Y - useful for increasing blood
 PT pressure and treating eating disorders such as anorexia nervosa.
 XX
 PS Example 9; Col 9; 7pp; English.
 XX
 CC The patent relates to a new group of peptides which have neuropeptide Y
 CC agonist action. The peptides have hypertensive activity, vasoconstricting
 CC activity, colon relaxing activity and gastric emptying diminution
 CC activity. They are of particular use in treatment of eating disorders
 CC such as anorexia nervosa. The present sequence is that of a peptide
 CC prepared in the Examples of the patent, but it does not appear to fit the
 CC generic formulae of the active compounds
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7
 |||
 Db 8 RQR 10

RESULT 61
 AAW49555
 ID AAW49555 standard; peptide; 11 AA.
 XX
 AC AAW49555;
 XX
 DT 05-JUN-1998 (first entry)

XX
 DE Human leucocyte antigen DQ4 binding peptide #446.
 XX
 KW Human leucocyte antigen; HLA-DQ4; combinatorial library;
 KW autoimmune disease; chronic articular rheumatism.
 XX
 OS Synthetic.
 XX
 PN JP08151396-A.
 XX
 PD 11-JUN-1996.
 XX
 PF 28-NOV-1994; 94JP-00292657.
 XX
 PR 28-NOV-1994; 94JP-00292657.
 XX
 PA (TEIJ) TEIJIN LTD.
 XX
 DR WPI; 1996-329479/33.
 XX
 PT HLA-binding oligopeptide and an immuno:regulator contg it - used in the
 PT treatment of auto:immune disease.
 XX
 PS Claim 4; Page 49; 61pp; Japanese.
 XX
 CC This peptide is an example of a peptide which binds to a human leucocyte
 CC antigen HLA-DQ4 molecule. The peptide was isolated from a phagemid
 CC combinatorial library comprising the sequence AAV05953, by screening with
 CC an HLA-DQ4 molecule. The peptide is used for the treatment of autoimmune
 CC disease, or especially for treatment of viral diseases
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7
 |||
 Db 6 RQR 8

RESULT 62

AAR96835

ID AAR96835 standard; peptide; 11 AA.

XX

AC AAR96835;

XX

DT 29-NOV-1996 (first entry)

XX

DE Human neurofilament triplet h fragment, homologous to Neisseria Iga-
 DE alphas.

XX

KW IgA protease precursor; IPP; bacterial polyprotein; autoimmune;

KW viral infection; rheumatoid arthritis; AIDS; meningococcal bacteria;

KW human neurofilament triplet h protein; Nfh; Neisseria gonorrhoeae; MS11.

XX

OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 1. .3
 FT /note= "identical to sequence in Neisseria gonorrhoeae
 FT Iga-alpha1"
 FT Region 5. .7
 FT /note= "identical to sequence in Neisseria gonorrhoeae
 FT Iga-alpha1"
 FT Region 10. .11
 FT /note= "identical to sequence in Neisseria gonorrhoeae
 FT Iga-alpha1"
 XX
 PN WO9609395-A2.
 XX
 PD 28-MAR-1996.
 XX
 PF 21-SEP-1995; 95WO-EP003726.
 XX
 PR 21-SEP-1994; 94DE-04433708.
 XX
 PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 XX
 PI Meyer TF, Pohlner J, Beck SC, Jose J, Woelk U, Lorenzen DR;
 PI Oetzelberger KB;
 XX
 DR WPI; 1996-188456/19.
 XX
 PT Medicaments for treating auto-immune or viral diseases - contg.
 PT substances interfering with bacterial poly:protein function.
 XX
 PS Claim 32; Fig 2; 117pp; German.
 XX
 CC The present sequence from human neurofilament triplet h protein has
 CC homology to a cleavage product from the Iga-alpha1 domain of the
 CC precursor of IgA-protease polyprotein (IPP) of Neisseria gonorrhoeae
 CC strain MS11. The Neisseria IPP has been implicated in rheumatoid
 CC arthritis and other auto-immune diseases. The polyprotein also activates
 CC proviruses, including HIV. Substances which interfere with the function
 CC of IPP from Neisseria will be useful for treating associated autoimmune
 CC diseases and viral infections. Peptides comprising the homology region
 CC sequences, whether from Neisseria or from humans, are claimed
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7
 |||
 Db 2 RQR 4

RESULT 63

AAR85318

ID AAR85318 standard; peptide; 11 AA.

XX
 AC AAR85318;
 XX
 DT 25-MAR-2003 (revised)
 DT 19-AUG-1996 (first entry)
 XX
 DE Human retinoic acid receptor RAR-beta (human liver HAP) peptide-2.
 XX
 KW HAP; liver; hepatoma; retinoic acid receptor; RAR-beta; psoriasis;
 KW atherosclerosis; rheumatoid arthritis.
 XX
 OS Homo sapiens.
 XX
 PN US5468617-A.
 XX
 PD 21-NOV-1995.
 XX
 PF 02-FEB-1994; 94US-00190555.
 XX
 PR 16-DEC-1987; 87US-00133687.
 PR 17-DEC-1987; 87US-00134130.
 PR 20-JUN-1988; 88US-00209009.
 PR 30-NOV-1988; 88US-00278136.
 PR 30-MAR-1989; 89US-00330405.
 PR 21-AUG-1991; 91US-00751612.
 PR 30-MAR-1992; 92US-00860577.
 PR 11-DEC-1992; 92US-00989902.
 PR 22-JUL-1993; 93US-00095706.
 XX
 PA (TIOL/) TIOLLAIS P.
 PA (DEJE/) DEJEAN A.
 PA (KRUS/) KRUST A.
 PA (PETK/) PETKOVICH M.
 PA (DTHE/) BLAUDIN DE THE H.
 PA (MARC/) MARCHIO A.
 PA (BRAN/) BRAND N.
 PA (CHAM/) CHAMBON P.
 XX
 PI Brand N, Chambon P, Blaudin De The H, Marchio A, Dejean A;
 PI Petkovich M, Krust A, Tiollais P;
 XX
 DR WPI; 1996-010094/01.
 XX
 PT Method for screening for retinoic acid receptor-beta (ant)agonists -
 PT useful for blood testing and for treatment of rheumatoid arthritis,
 PT psoriasis, atherosclerosis etc.
 XX
 PS Claim 7; Col 39-40; 35pp; English.
 XX
 CC This RAR-beta peptide-2 fragment is part of a protein which may be
 CC expressed recombinantly in bacterial host cells such as Escherichia coli
 CC TG-1. The protein, which is free from human, blood-derived protein, forms
 CC a complex with an agonist or antagonist. The protein may be used in a
 CC novel method for assaying a fluid for the presence of an agonist or
 CC antagonist to retinoic acid receptor, RAR-beta. (Updated on 25-MAR-2003
 CC to correct PF field.)
 XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKE 4
|||
Db 7 KKE 9

RESULT 64

AAW18499

ID AAW18499 standard; peptide; 11 AA.

XX

AC AAW18499;

XX

DT 19-FEB-1998 (first entry)

XX

DE Amino-terminal peptide 1 associated with novel helicase.

XX

KW Nucleic acid binding protein; helicase; leflunomide; assaying;
KW 4-(N-(4-trifluoromethylphenyl)-5-methyl-isoxazole; identification;
KW anticancer; antiatherosclerotic; immunosuppressant; sequencing;
KW antiinflammatory; antiviral; antifungal; antibacterial; treatment;
KW Alzheimer's disease; cancer; rheumatism; arthrosis; determination;
KW atherosclerosis; osteoporosis; acute infection; chronic infection;
KW autoimmune disease; diabetes; organ transplant; isolation;
KW amino-terminal.

XX

OS Homo sapiens.

XX

PN DE19545126-A1.

XX

PD 05-JUN-1997.

XX

PF 04-DEC-1995; 95DE-01045126.

XX

PR 04-DEC-1995; 95DE-01045126.

XX

PA (FARH) HOECHST AG.

XX

PI Kirschbaum B, Muellner S, Bartlett R;

XX

DR WPI; 1997-299388/28.

XX

PT New nucleic acid binding protein with helicase activity - is strongly
PT induced by leflunomide, used to isolate specific binding RNA and for
PT identifying substances with anticancer, antiviral etc. activities.

XX

PS Example 4; Page 15; 28pp; German.

XX

CC The present sequence is an amino-terminal peptide associated with a novel
CC nucleic acid binding protein with helicase activity, the mRNA of which
CC (or its translation products) is strongly expressed in presence of
CC leflunomide, i.e. 4-(N-(4-trifluoromethylphenyl)-5-methyl-isoxazole, or a
CC compound with similar activity. The helicase can be used in assay systems

CC to identify/discover anticancer, antiatherosclerotic, immunosuppressing,
CC antiinflammatory, antiviral, antifungal and antibacterial agents, e.g. to
CC treat Alzheimer's disease, cancer, rheumatism, arthrosis,
CC atherosclerosis, osteoporosis, acute/chronic infections, autoimmune
CC disease, diabetes and complications of organ transplants, and to isolate
CC or determine the sequences of specific binding RNA
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKE 4
|||
Db 9 KKE 11

RESULT 65

AAW24438

ID AAW24438 standard; peptide; 11 AA.

XX

AC AAW24438;

XX

DT 30-SEP-1997 (first entry)

XX

DE Nucleic acid (NA) binding peptide used in NA delivery to cells.

XX

KW Nucleic acid transporter; gene therapy; binding complex; lysis agent;

KW JTS-1; K8; alpha helix; endosome; lysosome; nucleus targeting.

XX

OS Synthetic.

XX

PN WO9640958-A1.

XX

PD 19-DEC-1996.

XX

PF 23-APR-1996; 96WO-US005679.

XX

PR 07-JUN-1995; 95US-00484777.

XX

PA (BAYU) BAYLOR COLLEGE MEDICINE.

XX

PI Smith LC, Sparrow JT, Woo SL;

XX

DR WPI; 1997-052345/05.

XX

PT Nucleic acid transporter useful in gene therapy - contains binding
PT complex associated with surface and nuclear ligands and lysis agent.

XX

PS Disclosure; Page 49; 125pp; English.

XX

CC AAW24434-W24459 are nucleic acid (NA) binding peptides, capable of both
CC condensing and stabilising a NA. The peptides can be conjugated to a
CC lytic peptide to form a nucleic acid transporter system. The lysis agent
CC forms an alpha-helical structure. The transporter system is used to
CC deliver nucleic acid to a cell and for treating humans by gene therapy.

CC By taking advantage of the characteristics of both the lysis agents and
CC the binding molecules, delivery of the nucleic acid is enhanced. Specific
CC lysis agents are capable of releasing the nucleic acid into the cellular
CC interior from the endosome. Release is efficient without
CC endosomal/lysosomal degradation. Once released the binding complexes help
CC target the nucleic acid to the nucleus

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3

|||

Db 3 AKK 5

RESULT 66

AAW34642

ID AAW34642 standard; peptide; 11 AA.

XX

AC AAW34642;

XX

DT 02-MAR-1998 (first entry)

XX

DE Control peptide.

XX

KW Occludin; inhibitor; human; drug absorption; drug delivery; gene therapy;

KW tissue permeability; cell adhesion; antibody.

XX

OS Synthetic.

XX

PN WO9733605-A1.

XX

PD 18-SEP-1997.

XX

PF 14-MAR-1997; 97WO-US005809.

XX

PR 15-MAR-1996; 96US-0013625P.

XX

PA (UYA) UNIV YALE.

XX

PI Anderson JM, Van Itallie CM;

XX

DR WPI; 1997-470640/43.

XX

PT Isolated human occludin protein - useful for increasing drug delivery

PT across endothelial or epithelial barriers, or for reducing tissue

PT permeability.

XX

PS Disclosure; Page 36; 49pp; English.

XX

CC This control peptide was used in experiments to demonstrate inhibition of
CC occludin-dependent intercellular adhesion using extracellular loop
CC peptides corresponding to the N-terminal half of occludin extracellular
CC loop 1 (see AAW34639) and the C-terminal half of extracellular loop 1

CC (see AAW34640. Inhibitors of human occludin inhibitors can be used to
CC enhance delivery of drugs (or gene therapy vectors) by increasing
CC absorption across endothelial or epithelial barriers, i.e. transmucosal
CC or transvascular drug delivery. Inhibitors include occludin surface loop
CC peptides that inhibit adhesion and/or barrier properties, or antibodies
CC that interact with occludin or occludin receptors
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RKD 9
|||
Db 7 RKD 9

RESULT 67

AAW09909

ID AAW09909 standard; peptide; 11 AA.

XX

AC AAW09909;

XX

DT 16-OCT-1997 (first entry)

XX

DE Prostate specific membrane antigen peptide PSM-P26.

XX

KW Prostate specific membrane antigen; PSMA; prostate specific antigen; PSA;

KW prostate cancer; adoptive cellular immunotherapy; therapy; vaccine.

XX

OS Homo sapiens.

XX

PN WO9704802-A1.

XX

PD 13-FEB-1997.

XX

PF 29-JUL-1996; 96WO-US012389.

XX

PR 31-JUL-1995; 95US-00509254.

XX

PA (PACI-) PACIFIC NORTHWEST CANCER FOUND.

XX

PI Murphy GP, Boynton AL, Tjoa BA;

XX

DR WPI; 1997-145375/13.

XX

PT Use of dendritic cells for prostate cancer immuno:therapy - the cells are

PT exposed to prostate cancer antigen, then administered to the patient

PT where they activate and proliferate T-cells.

XX

PS Claim 3; Page 47; 69pp; English.

XX

CC Peptide PSM-P26 (AAW09909) corresponds to amino acid residues 398-408 of

CC prostate specific membrane antigen (PSMA). A method for producing a

CC cancer growth inhibiting response comprises exposing human dendritic

CC cells (DCs) to PSM-P26 or other PSMA or prostate specific antigen

CC peptides (see also AAW09889-908 and AAW09910-26), and then administering
CC the DCs to a prostate cancer patient to activate T cell responses in
CC vivo. Alternatively, the T cell response is activated in vitro and the T
CC cells are then administered to the patient. In either case, the DCs are
CC used to elicit an immunotherapeutic growth inhibiting response against a
CC primary or metastatic prostate tumour. PSM-P26 was selected to be
CC presented by DCs to activate T cells of a patient which match the A11
CC haplotype

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKE 4

|||

Db 9 KKE 11

RESULT 68

AAW10140

ID AAW10140 standard; peptide; 11 AA.

XX

AC AAW10140;

XX

DT 25-MAR-2003 (revised)

DT 02-OCT-1997 (first entry)

XX

DE Hepatitis C virus peptide antigen IIA.

XX

KW Antibody; HCV; immunoassay; vaccine; mimic.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "H or a linker arm by which the peptide can be
FT attached to a carrier or solid phase comprising at least
FT one amino acid and as many as 60, most frequently 1-20
FT amino acids, such as Cys, Lys, Tyr, Glu or Asp, or
FT chemical groups such as biotin or thioglycolic acid; can
FT be modified by acetylation"

FT Modified-site 11

FT /note= "A bond or a linker arm by which the peptide can
FT be attached to a carrier or solid phase comprising at
FT least one amino acid and as many as 60 amino acids, most
FT frequently 1-10 amino acids, such as Cys, Lys, Tyr, Asp,
FT or chemical groups such as biotin or thioglycolic acid;
FT and attached on to that is NH2, OH or a linkage involving
FT either of these two groups"

XX

PN EP754704-A2.

XX

PD 22-JAN-1997.

XX

PF 14-DEC-1990; 96EP-00201157.

XX
 PR 14-DEC-1990; 90EP-00124241.
 XX
 PA (INNO-) INNOGENETICS NV.
 XX
 PI Deleys RJ, Pollet D, Maertens G, Van Heuverswyn H;
 XX
 DR WPI; 1997-089256/09.
 XX
 PT Hepatitis C virus peptide mimics - for use in immunoassays, vaccines,
 PT etc.
 XX
 PS Claim 2; Page 38; 65pp; English.
 XX
 CC The present sequence represents a novel synthetic Hepatitis C virus (HCV)
 CC antigen IIA for the detection of antibodies. The peptide contains
 CC modifications at the N- and C-terminal (see features table) with the
 CC condition that if the modification represents an amino acid(s), that they
 CC are different from any naturally occurring HCV flanking regions. The
 CC peptide represents an HCV peptide mimic and may be used as an immunoassay
 CC reagent for detecting antibodies to HCV; for incorporation into vaccines
 CC against HCV; and for raising antibodies against HCV. (Updated on 25-MAR-
 CC 2003 to correct PF field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QRK 8
 |||
 Db 1 QRK 3

RESULT 69
 AAW62116
 ID AAW62116 standard; peptide; 11 AA.
 XX
 AC AAW62116;
 XX
 DT 16-SEP-1998 (first entry)
 XX
 DE Human MDM2 binding peptide 5.
 XX
 KW Identification; ligand; biological activity; target-binding;
 KW drug screening; library; inhibitory ligand.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9819162-A1.
 XX
 PD 07-MAY-1998.
 XX
 PF 31-OCT-1997; 97WO-US019638.
 XX

PR 31-OCT-1996; 96US-00740671.

XX

PA (NOVA-) NOVALON PHARM CORP.

XX

PI Fowlkes DM, Kay BK, Frelinger JA, Hyde-Deruyscher RP;

XX

DR WPI; 1998-272389/24.

XX

PT Identifying ligands which mediate biological activity of a protein - by
PT identifying target-binding ligands and screening a library for ligands
PT which inhibit target-binding ligand mediated activity.

XX

PS Example 3; Page 93; 143pp; English.

XX

CC A method has been developed for identifying a ligand which mediates the
CC biological activity of a target protein (T) by inhibiting the binding of
CC (T) to a binding partner. The method comprises: (a) screening a first
CC combinatorial library comprising first member ligands for binding to the
CC target-binding ligands (TBLs), to identifying one or more TBLs; (b)
CC screening a second library comprising second member ligands for the
CC ability to inhibit the binding of one or more of the TBLs to the target
CC protein, and so obtaining one or more inhibitory ligands; and (c)
CC determining which of the inhibitory ligands can mediate a biological
CC activity of the target protein. The present sequence represents a
CC potential binding peptide for human MDM2 from an example of the present
CC invention. The method can be used for identifying drugs which can mediate
CC the biological activity of a target protein. It can be used to identify
CC the biological activity of a target protein whose biological function is
CC not known and perhaps cannot be determined directly. The method can also
CC be used to identify new inhibitory ligands of specific target proteins.
CC The method provides high throughput screens which are essentially
CC identical for similar and dissimilar targets, bypassing the need to
CC develop distinct assays for biochemically diverse targets

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 9.8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKE 4

|||

Db 8 KKE 10

RESULT 70

AAW66523

ID AAW66523 standard; peptide; 11 AA.

XX

AC AAW66523;

XX

DT 25-NOV-1998 (first entry)

XX

DE Amphiphilic peptide.

XX

KW magainin; analogue; antimicrobial; antitumour; wound healing; CPF;

KW amphiphilic; XPF peptide.

XX
 OS Synthetic.
 XX
 PN US5792831-A.
 XX
 PD 11-AUG-1998.
 XX
 PF 17-NOV-1994; 94US-00343882.
 XX
 PR 08-FEB-1990; 90US-00476629.
 PR 14-MAY-1990; 90US-00522688.
 PR 28-APR-1992; 92US-00874685.
 PR 05-OCT-1993; 93US-00133740.
 XX
 PA (MAGA-) MAGAININ PHARM INC.
 XX
 PI Maloy WL;
 XX
 DR WPI; 1998-456190/39.
 XX
 PT Magainin peptide analogues - useful as antimicrobial or antitumour
 PT agents, etc.
 XX
 PS Disclosure; Col 20; 25pp; English.
 XX
 CC The invention relates to analogues of a magainin I or II, D-form
 CC analogues, deletion analogues or related peptides. It also relates to
 CC basic polypeptides having at least 16 amino acids, including at least 8
 CC hydrophobic amino acids and at least 8 hydrophilic amino acids. The
 CC peptides may be used as antimicrobial agents, antiviral agents,
 CC antibiotics, antitumour agents, antiparasitic agents, spermicides,
 CC preservatives or sterilants, or agents for promoting wound healing. The
 CC present sequence represents a specific example of a peptide disclosed in
 CC the specification
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
 |||
 Db 1 AKK 3

RESULT 71

AAW80589

ID AAW80589 standard; peptide; 11 AA.

XX

AC AAW80589;

XX

DT 18-DEC-1998 (first entry)

XX

DE src-family tyrosine kinase peptide fragment.

XX

KW src-family tyrosine kinase; serine phosphorylation-mediated degradation;

KW mutation; T cell activation; immune response; screening; cancerous cell;
KW therapy; immunity; allogenic transplant; xenogeneic organ transplant.

XX

OS Mus sp.

XX

FH Key Location/Qualifiers

FT Misc-difference 8

FT /note= "can be replaced with Ala"

FT Misc-difference 9

FT /note= "can be replaced with Ala"

XX

PN WO9846996-A2.

XX

PD 22-OCT-1998.

XX

PF 10-APR-1998; 98WO-IB000801.

XX

PR 11-APR-1997; 97US-0041878P.

XX

PA (ROBA-) ROBERTS RES INST JOHN P.

XX

PI Madrenas J;

XX

DR WPI; 1998-583294/49.

XX

PT Detection of levels of T cell activation - by measuring increase in
PT amount of serine phosphorylated Ick relative to total Ick as indicative
PT of increased T cell activation.

XX

PS Claim 23; Page 27; 48pp; English.

XX

CC This represents a peptide fragment of the src-family tyrosine kinase
CC polypeptide. The invention provides src-family tyrosine kinase peptide
CC fragments (AAW80586 to AAW80591), which on mutation reduces the serine
CC phosphorylation-mediated degradation of the polypeptide. The mutation
CC could be a mutation of the serine residue located at the amino terminus
CC to alanine and/or could be a mutation that results in a leucine- leucine
CC to alanine-alanine change in the polypeptide. The invention also provides
CC methods for detecting the level of T cell activation; for detecting a
CC compound that modulates T cell activation; and for generating a src-
CC family tyrosine kinase polypeptide that has a reduced level of serine
CC phosphorylation-mediated degradation. The methods can be used for the
CC rapid detection of an antigen-specific immune response. They can also be
CC used for screening candidate therapeutic compounds and protocols for the
CC efficacy in either stimulating or blocking the antigen-specific immune
CC response. Identification and development of such compounds and protocols
CC is useful for enhancing, decreasing or preventing antigen- specific
CC immune responses. Therapies which enhance the immune response aid in the
CC development of immunity to antigens derived from pathogens and cancerous
CC cells. Therapies which prevent or decrease the development of an antigen-
CC specific immune response are useful in preventing an immune response to
CC antigens derived from e.g. allogenic or xenogeneic organ transplants

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 9.8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RKD 9
|||
Db 1 RKD 3

RESULT 72

AAW64653

ID AAW64653 standard; peptide; 11 AA.

XX

AC AAW64653;

XX

DT 23-OCT-1998 (first entry)

XX

DE Synthetic SEB-related peptide (position 51-61).

XX

KW Enterotoxin B; SEB; pyrogenic exotoxin; PET; protective immunity;

KW toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;

KW therapeutic; vaccine; food poisoning.

XX

OS Synthetic.

OS Staphylococcus aureus.

XX

PN WO9829444-A1.

XX

PD 09-JUL-1998.

XX

PF 30-DEC-1997; 97WO-IL000438.

XX

PR 30-DEC-1996; 96IL-00119938.

XX

PA (YISS) YISSUM RES & DEV CO.

XX

PI Kaempfer R, Arad G;

XX

DR WPI; 1998-388042/33.

XX

PT New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.

PT antagonising toxin-mediated activation of T cells and prevention or

PT treatment of toxic shock caused by exotoxin(s).

XX

PS Example 2; Page 38; 68pp; English.

XX

CC AAW64636-W64657 are peptides homologous to the amino acid sequence of a

CC fragment of a pyrogenic exotoxin (PET), and derivatives of the peptide

CC capable of eliciting protective immunity against toxic shock induced by

CC PET or by a mixture of PETs. Such peptides are also capable of

CC antagonising toxin-mediated activation of T-cells, inhibiting expression

CC of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or TNF-

CC beta genes. The peptides may be used to prepare therapeutics or vaccines

CC for the treatment of prophylaxis of toxin-mediated activation of T cells

CC and eliciting protective immunity against toxic shock induced by PETs.

CC They can also be used for the treatment of harmful effects (especially

CC food poisoning) and toxic shock caused by PET. Antiserum to the peptides

CC can also be used for alleviating toxic shock induced by PET

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KDT 10
|||
Db 4 KDT 6

RESULT 73

AAW51825

ID AAW51825 standard; peptide; 11 AA.

XX

AC AAW51825;

XX

DT 13-OCT-1998 (first entry)

XX

DE Peptide YY analogue #26.

XX

KW peptide YY; cell proliferation; nutrient transport; lipolysis;

KW electrolyte secretion; anti-secretory; intestinal water; antimotility.

XX

OS Synthetic.

OS Mammalia.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "N-terminal acetyl"

FT Modified-site 11

FT /note= "C-terminal amide"

XX

PN WO9820885-A1.

XX

PD 22-MAY-1998.

XX

PF 13-NOV-1996; 96WO-US018374.

XX

PR 13-NOV-1996; 96WO-US018374.

XX

PA (UYCI-) UNIV CINCINNATI.

XX

PI Balasubramaniam A;

XX

DR WPI; 1998-322327/28.

XX

PT New analogue(s) of peptide YY - used, e.g. to control cell proliferation,

PT nutrient transport, lipolysis and intestinal water and electrolyte

PT secretion.

XX

PS Disclosure; Page 17; 54pp; English.

XX

CC The invention relates to peptide YY analogues which may be used e.g. for

CC decreasing excess intestinal water and electrolyte secretion in mammals,

CC to regulate cell proliferation (especially intestinal cell

CC proliferation), to increase nutrient transport, to regulate lipolysis and

CC to regulate blood flow. The peptides exhibit antisecretory and
CC antimotility properties and are especially useful in treatment of
CC gastrointestinal disorders associated with excess intestinal electrolyte
CC and water secretion as well as decreased absorption. The new peptides are
CC truncated versions of peptide YY. They interact solely with peptide YY
CC receptors and not with homologous receptors such as NPY Y1 and Y3, thus
CC minimising unwanted (ant)agonist side reactions. The present sequence
CC represents a peptide YY analogue

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 9.8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7

|||

Db 8 RQR 10

RESULT 74

AAW84029

ID AAW84029 standard; peptide; 11 AA.

XX

AC AAW84029;

XX

DT 05-FEB-1999 (first entry)

XX

DE Human CYP3A4 specific synthetic peptide fragment 18.

XX

KW CYP3A4; epitope; anti-peptide antibody; enzyme; therapeutic agent;

KW cytochrome P450; gene expression; tissue localisation; inhibitory;

KW affinity purification; human.

XX

OS Synthetic.

OS Homo sapiens.

XX

PN WO9844939-A1.

XX

PD 15-OCT-1998.

XX

PF 09-APR-1998; 98WO-US007165.

XX

PR 10-APR-1997; 97US-0043230P.

XX

PA (MERI) MERCK & CO INC.

XX

PI Lu AYH, Wang RW;

XX

DR WPI; 1998-609899/51.

XX

PT New antibodies to human CYP3A4 - are specific relative to other human

PT P450 enzymes, produced using peptides specific for human CYP3A4.

XX

PS Example 2; Page 24; 58pp; English.

XX

CC Sequences AAW84012 to AAW84039 represent synthetic peptides specific to

CC human CYP3A4. The peptides are fragments contained within the peptide
CC AAW84012 or AAW84013 comprising an inhibitory epitope. The invention
CC provides anti-peptide antibodies raised against such human CYP3A4
CC specific peptides in relation to other human P450 enzymes and inhibit
CC human CYP3A4 activity. The inhibitory anti-peptide antibodies are used
CC for evaluating the role of human CYP3A4 in mediating in vitro metabolism
CC of therapeutic agents. In addition, the antibodies can be used for
CC cytochrome P450 epitope investigation, gene expression and regulation,
CC tissue localisation, affinity purification for CYP3A4 and many other
CC studies
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 DTQ 11
| | |
Db 1 DTQ 3

RESULT 75

AAW84023

ID AAW84023 standard; peptide; 11 AA.

XX

AC AAW84023;

XX

DT 05-FEB-1999 (first entry)

XX

DE Human CYP3A4 specific synthetic peptide fragment 12.

XX

KW CYP3A4; epitope; anti-peptide antibody; enzyme; therapeutic agent;

KW cytochrome P450; gene expression; tissue localisation; inhibitory;

KW affinity purification; human.

XX

OS Synthetic.

OS Homo sapiens.

XX

PN WO9844939-A1.

XX

PD 15-OCT-1998.

XX

PF 09-APR-1998; 98WO-US007165.

XX

PR 10-APR-1997; 97US-0043230P.

XX

PA (MERI) MERCK & CO INC.

XX

PI Lu AYH, Wang RW;

XX

DR WPI; 1998-609899/51.

XX

PT New antibodies to human CYP3A4 - are specific relative to other human

PT P450 enzymes, produced using peptides specific for human CYP3A4.

XX

PS Example 2; Page 24; 58pp; English.

XX
CC Sequences AAW84012 to AAW84039 represent synthetic peptides specific to
CC human CYP3A4. The peptides are fragments contained within the peptide
CC AAW84012 or AAW84013 comprising an inhibitory epitope. The invention
CC provides anti- peptide antibodies raised against such human CYP3A4
CC specific peptides in relation to other human P450 enzymes and inhibit
CC human CYP3A4 activity. The inhibitory anti-peptide antibodies are used
CC for evaluating the role of human CYP3A4 in mediating in vitro metabolism
CC of therapeutic agents. In addition, the antibodies can be used for
CC cytochrome P450 epitope investigation, gene expression and regulation,
CC tissue localisation, affinity purification for CYP3A4 and many other
CC studies
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 DTQ 11
|||
Db 7 DTQ 9

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Job time : 46.3077 secs

OM protein - protein search, using sw model

Run on: April 8, 2004, 15:30:08 ; Search time 11.3077 Seconds
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Perfect score: 11
Sequence: 1 AKKERQRKDTQ 11

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 389414 seqs, 51625971 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8542

Minimum DB seq length: 11

Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	4	36.4	11	2	US-08-747-137-63	Sequence 63, Appl			
5	4	36.4	11	3	US-09-100-930A-10	Sequence 10, Appl			
6	3	27.3	11	1	US-08-193-521-18	Sequence 18, Appl			
7	3	27.3	11	1	US-08-197-793-8	Sequence 8, Appli			
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10	3	27.3	11	1	US-08-306-546C-25	Sequence 25, Appl			
11	3	27.3	11	1	US-08-434-120-112	Sequence 112, App			

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17	3	27.3	11	1	US-08-411-727-18	Sequence 18, Appl
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100	3	27.3	11	4	US-09-941-611-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1

US-08-185-448-5

; Sequence 5, Application US/08185448

; Patent No. 5580747

; GENERAL INFORMATION:

; APPLICANT: SHULTZ, JOHN W.

; APPLICANT: WHITE, DOUGLAS H.

; TITLE OF INVENTION: NON-RADIOACTIVE KINASE,

; TITLE OF INVENTION: PHOSPHATASE AND PROTEASE ASSAY

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: ANDRUS, SCEALES, STARKE & SAWALL

; STREET: 100 E. WISCONSIN AVENUE, SUITE 1100

; CITY: MILWAUKEE

; STATE: WISCONSIN

; COUNTRY: USA

; ZIP: 53202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

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;   OPERATING SYSTEM:  PC-DOS/MS-DOS
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;   SOFTWARE:  #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/185,448
;   FILING DATE:  21-JAN-1994
;   CLASSIFICATION:  435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  US 07/791,928
;   FILING DATE:  12-NOV-1991
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  SARA, CHARLES S
;   REGISTRATION NUMBER:  30492
;   REFERENCE/DOCKET NUMBER:  F.3347-1
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  (608) 255-2022
;   TELEFAX:  (608) 255-2182
;   TELEX:  26832 ANDSTARK
;   INFORMATION FOR SEQ ID NO:  5:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  11 amino acids
;   TYPE:  amino acid
;   TOPOLOGY:  linear
;   MOLECULE TYPE:  peptide
;   FEATURE:
;   NAME/KEY:  Binding-site
;   LOCATION:  1
;   OTHER INFORMATION:  /label= LABEL
;   OTHER INFORMATION:  /note= "LOCATION OF LISSAMINE RHODAMINE
;   OTHER INFORMATION:  DETECTION TAG"
US-08-185-448-5

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Query Match          36.4%;  Score 4;  DB 1;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 2.1e+02;
Matches      4;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

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Qy      5 RQRK 8
        ||||
Db      3 RQRK 6

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RESULT 2

US-08-476-405A-10

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; Sequence 10, Application US/08476405A
; Patent No. 5776459
; GENERAL INFORMATION:
;   APPLICANT:  Vandembark, Arthur A.
;   TITLE OF INVENTION:  Method of Treatment Using TCR VBeta5 Peptides
;   NUMBER OF SEQUENCES:  27
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  Connective Therapeutics, Inc.
;   STREET:  3400 West Bayshore Road
;   CITY:  Palo Alto
;   STATE:  California
;   COUNTRY:  USA
;   ZIP:  94303
;   COMPUTER READABLE FORM:

```

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,405A
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/059,020
; FILING DATE: 16-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,612
; FILING DATE: 16-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/708,022
; FILING DATE: 31-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/554,529
; FILING DATE: 19-JUL-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/467,577
; FILING DATE: 19-JAN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/382,804
; FILING DATE: 19-JUL-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowin, David A.
; REGISTRATION NUMBER: 29,326
; REFERENCE/DOCKET NUMBER: 886 P15
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-2800
; TELEFAX: 415-843-2899
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-476-405A-10

```

```

Query Match          36.4%; Score 4; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      4 ERQR 7
        ||||
Db      7 ERQR 10

```

```

RESULT 3
US-08-476-405A-11
; Sequence 11, Application US/08476405A
; Patent No. 5776459
; GENERAL INFORMATION:
; APPLICANT: Vandenbark, Arthur A.

```



```

; TITLE OF INVENTION: Method of Treatment Using TCR VBeta5 Peptides
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Connective Therapeutics, Inc.
; STREET: 3400 West Bayshore Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,405A
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/059,020
; FILING DATE: 16-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,612
; FILING DATE: 16-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/708,022
; FILING DATE: 31-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/554,529
; FILING DATE: 19-JUL-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/467,577
; FILING DATE: 19-JAN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/382,804
; FILING DATE: 19-JUL-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowin, David A.
; REGISTRATION NUMBER: 29,326
; REFERENCE/DOCKET NUMBER: 886 P15
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-2800
; TELEFAX: 415-843-2899
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-476-405A-11

```

```

Query Match          36.4%; Score 4; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 4 ERQR 7

Db ||||
 7 ERQR 10

RESULT 4

US-08-747-137-63

; Sequence 63, Application US/08747137
; Patent No. 5945033
; GENERAL INFORMATION:
; APPLICANT: YEN, Richard C.K.
; TITLE OF INVENTION: NON-CROSSLINKED PROTEIN PARTICLES FOR
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC USE
; NUMBER OF SEQUENCES: 184
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/747,137
; FILING DATE: 12-NOV-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,546
; FILING DATE: 14-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/069,831
; FILING DATE: 01-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/959,560
; FILING DATE: 13-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/641,720
; FILING DATE: 15-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 016197-000840US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant

US-08-747-137-63

Query Match 36.4%; Score 4; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQRK 8
||||
Db 3 RQRK 6

RESULT 5

US-09-100-930A-10

; Sequence 10, Application US/09100930A

; Patent No. 6248549

; GENERAL INFORMATION:

; APPLICANT: Van Eyk, Jennifer E.

; APPLICANT: Mak, Alan S.

; APPLICANT: Cote, Graham P.

; TITLE OF INVENTION: Methods of Modulating Muscle Contraction

; FILE REFERENCE: 1997-021-03US

; CURRENT APPLICATION NUMBER: US/09/100,930A

; CURRENT FILING DATE: 1998-06-22

; PRIOR APPLICATION NUMBER: 60/050,478

; PRIOR FILING DATE: 1997-06-23

; PRIOR APPLICATION NUMBER: 60/089,505

; PRIOR FILING DATE: 1998-06-16

; NUMBER OF SEQ ID NOS: 26

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 10

; LENGTH: 11

; TYPE: PRT

; ORGANISM: Unknown

; FEATURE:

; NAME/KEY: PEPTIDE

; LOCATION: (1)..(11)

; OTHER INFORMATION: Residues 423 to 433 of chicken gizzard caldesmon

; NAME/KEY: PEPTIDE

; LOCATION: (11)

; OTHER INFORMATION: Targeted Ser phospho-amino acid

US-09-100-930A-10

Query Match 36.4%; Score 4; DB 3; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKKE 4
||||
Db 7 AKKE 10

RESULT 6

US-08-193-521-18

; Sequence 18, Application US/08193521

; Patent No. 5470950

; GENERAL INFORMATION:

; APPLICANT: Maloy, W. Lee

; APPLICANT: Kari, U. Prasad

; APPLICANT: Williams, Jon I.

; TITLE OF INVENTION: Biologically Active Peptide

; TITLE OF INVENTION: Compositions and Uses Therefor

```

; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
; ADDRESSEE: Cecchi & Stewart
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: DW4.V2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/193,521
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/870,960
; FILING DATE:
; APPLICATION NUMBER: 07/760,054
; FILING DATE: 13-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliot M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 421250-161
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: May be a C-terminal amide,
; OTHER INFORMATION: and/or may be acetylated at
; OTHER INFORMATION: N-terminus.
US-08-193-521-18

```

```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 AKK 3
      |||
Db      1 AKK 3

```

```

RESULT 7
US-08-197-793-8
; Sequence 8, Application US/08197793
; Patent No. 5510461
; GENERAL INFORMATION:

```

```

; APPLICANT: Meuer, S.
; APPLICANT: Schraven, B.
; APPLICANT: Schoenhaut, D.
; APPLICANT: Ratnofsky, S.
; TITLE OF INVENTION: pp32: A Newly Identified CD45-Associated
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, SUITE 510
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/197,793
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/688,019;
; FILING DATE: 19-APR-1991
; APPLICATION NUMBER: 08/004,199
; FILING DATE: 13-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A., Jr.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: BBI-006CNCP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-197-793-8

```

```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      4 ERQ 6
      |||
Db      9 ERQ 11

```

```

RESULT 8
US-08-116-733-32
; Sequence 32, Application US/08116733
; Patent No. 5516632
; GENERAL INFORMATION:

```

; APPLICANT: PALKER, Thomas J.
 ; APPLICANT: HAYNES, Barton F.
 ; TITLE OF INVENTION: SYNTHETIC PEPTIDES
 ; NUMBER OF SEQUENCES: 46
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: NIXON & VANDERHYE P.C.
 ; STREET: 1100 NORTH GLEBE ROAD
 ; CITY: ARLINGTON
 ; STATE: VIRGINIA
 ; COUNTRY: U.S.A.
 ; ZIP: 22201-4714
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/116,733
 ; FILING DATE: 07-SEP-1993
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: WILSON, MARY J.
 ; REGISTRATION NUMBER: 32,955
 ; REFERENCE/DOCKET NUMBER: 1579-33
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703) 816-4000
 ; TELEFAX: (703) 816-4100
 ; TELEX: 200797 NIXN UR
 ; INFORMATION FOR SEQ ID NO: 32:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 11 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-08-116-733-32

Query Match 27.3%; Score 3; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
 |||
 Db 2 AKK 4

RESULT 9

US-08-329-151-26

; Sequence 26, Application US/08329151
 ; Patent No. 5604203
 ; GENERAL INFORMATION:
 ; APPLICANT: Balasubramaniam, A.
 ; TITLE OF INVENTION: ANALOGS OF PEPTIDE YY AND USES
 ; TITLE OF INVENTION: THEREOF
 ; NUMBER OF SEQUENCES: 30
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson
 ; STREET: 225 Franklin Street

```

; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/329,151
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/038,534
; FILING DATE: 3/29/93
; APPLICATION NUMBER: 08/109,326
; FILING DATE: 08/19/93
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00537/105001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11
; TYPE: amino acid
; STRANDEDNESS: N/A
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: The sequence has an acetylated N-terminus
; OTHER INFORMATION: (i.e., N--Ac), rather than an amino N-terminus
(i.e., H2N-).
; OTHER INFORMATION: has an amide C-terminus (i.e., CO-NH2), rather than a
carboxyl
; OTHER INFORMATION: (i.e., CO-OH).
US-08-329-151-26

```

```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      5 RQR 7
      |||
Db      8 RQR 10

```

```

RESULT 10
US-08-306-546C-25
; Sequence 25, Application US/08306546C
; Patent No. 5605797
; GENERAL INFORMATION:
; APPLICANT: Friderici, Karen
; APPLICANT: Jones, Margaret

```

```

; APPLICANT: Chen, Hong
; APPLICANT: Cavanagh, Kevin
; TITLE OF INVENTION: Bovine Beta-Mannosidase Gene and Methods
; TITLE OF INVENTION: of Use
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
; STREET: P.O. Box 828
; CITY: Bloomfield Hills
; STATE: Michigan
; COUNTRY: USA
; ZIP: 48303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/306,546C
; FILING DATE: September 15, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, DeAnn F.
; REGISTRATION NUMBER: 36,683
; REFERENCE/DOCKET NUMBER: 6550-00003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810)641-1600
; TELEFAX: (810)641-0270
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-306-546C-25

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```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      8 KDT 10
      |||
Db      2 KDT 4

```

RESULT 11

US-08-434-120-112

; Sequence 112, Application US/08434120

; Patent No. 5635479

; GENERAL INFORMATION:

; APPLICANT: Baker, Margaret A.

; APPLICANT: Jacob, Leonard S.

; APPLICANT: Maloy, W. Lee

; TITLE OF INVENTION: Treatment of Gynecological

; TITLE OF INVENTION: Malignancies with

; TITLE OF INVENTION: Biologically Active Peptides

; NUMBER OF SEQUENCES: 117


```

;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  Carella, Byrne, Bain, Gilfillan,
;   ADDRESSEE:  Cecchi & Stewart
;   STREET:    6 Becker Farm Road
;   CITY:      Roseland
;   STATE:     New Jersey
;   COUNTRY:   USA
;   ZIP:       07068
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: 3.5 inch diskette
;   COMPUTER:   IBM PS/2
;   OPERATING SYSTEM: PC-DOS
;   SOFTWARE:   DW4.V2
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/434,120
;   FILING DATE:
;   CLASSIFICATION:  514
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/297,950
;   FILING DATE:
;   APPLICATION NUMBER:  US/08/226,108
;   FILING DATE:
;   APPLICATION NUMBER:  US/07/937,462
;   FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;   NAME:        Olstein, Elliot M.
;   REGISTRATION NUMBER:  24,025
;   REFERENCE/DOCKET NUMBER:  421250-194
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:   201-994-1700
;   TELEFAX:     201-994-1744
;   INFORMATION FOR SEQ ID NO: 112:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:      11 amino acids
;   TYPE:         amino acid
;   STRANDEDNESS:
;   TOPOLOGY:    linear
;   MOLECULE TYPE:  peptide
US-08-434-120-112

```

```

Query Match          27.3%;  Score 3;  DB 1;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 2.3e+03;
Matches      3;  Conservative    0;  Mismatches    0;  Indels      0;  Gaps      0;

```

```

Qy          1 AKK 3
            |||
Db          1 AKK 3

```

```

RESULT 12
US-08-486-057B-16
; Sequence 16, Application US/08486057B
; Patent No. 5650494
;   GENERAL INFORMATION:
;   APPLICANT:  Cerletti, Nico
;   APPLICANT:  McMaster, Gary K.
;   APPLICANT:  Cox, David

```

; APPLICANT: Schmitz, Albert
 ; APPLICANT: Meyhack, Bernd
 ; TITLE OF INVENTION: Process for Refolding Recombinantly
 ; TITLE OF INVENTION: Produced TGF-beta-like Proteins
 ; NUMBER OF SEQUENCES: 43
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Henry P. No. 5650494ak
 ; STREET: 520 White Plains Road, P.O. Box 2005
 ; CITY: Tarrytown
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10591-9005
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/486,057B
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/201,703
 ; FILING DATE: 25-FEB-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/960,309
 ; FILING DATE: 13-OCT-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/621,502
 ; FILING DATE: 03-DEC-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: GB 8927546.5
 ; FILING DATE: 06-DEC-1989
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: No. 5650494ak, Henry P.
 ; REGISTRATION NUMBER: 33200
 ; REFERENCE/DOCKET NUMBER: 4-17861/+/Cont3
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (908) 277-5110
 ; TELEFAX: (908) 277-4306
 ; INFORMATION FOR SEQ ID NO: 16:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 11 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: not relevant
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: peptide
 US-08-486-057B-16

Query Match 27.3%; Score 3; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 DTQ 11
 |||
 Db 1 DTQ 3

RESULT 13
 US-08-465-325-111
 ; Sequence 111, Application US/08465325
 ; Patent No. 5686563
 ; GENERAL INFORMATION:
 ; APPLICANT: Magainin Pharmaceuticals Inc.
 ; APPLICANT: 5110 Campus Drive
 ; APPLICANT: Plymouth Meeting, PA 19462
 ; TITLE OF INVENTION: Biologically Active Peptides Having
 ; TITLE OF INVENTION: N-Terminal Substitutions
 ; NUMBER OF SEQUENCES: 153
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
 ; ADDRESSEE: Dunner
 ; STREET: 1300 I. Street, N.W. Suite 700
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20005-3315
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/465,325
 ; FILING DATE: 05-JUN-1995
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/184,462
 ; FILING DATE: 18-JAN-94
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/891,201
 ; FILING DATE: 01-JUN-92
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Fordis, Jean B
 ; REGISTRATION NUMBER: 32,984
 ; REFERENCE/DOCKET NUMBER: 05387.0021-03000
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 408-4000
 ; TELEFAX: (202) 408-4400
 ; INFORMATION FOR SEQ ID NO: 111:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 11 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-08-465-325-111

Query Match 27.3%; Score 3; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
 |||

RESULT 14

US-08-465-325-122

; Sequence 122, Application US/08465325

; Patent No. 5686563

; GENERAL INFORMATION:

; APPLICANT: Magainin Pharmaceuticals Inc.

; APPLICANT: 5110 Campus Drive

; APPLICANT: Plymouth Meeting, PA 19462

; TITLE OF INVENTION: Biologically Active Peptides Having

; TITLE OF INVENTION: N-Terminal Substitutions

; NUMBER OF SEQUENCES: 153

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &

; ADDRESSEE: Dunner

; STREET: 1300 I. Street, N.W. Suite 700

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20005-3315

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/465,325

; FILING DATE: 05-JUN-1995

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/184,462

; FILING DATE: 18-JAN-94

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/891,201

; FILING DATE: 01-JUN-92

; ATTORNEY/AGENT INFORMATION:

; NAME: Fordis, Jean B

; REGISTRATION NUMBER: 32,984

; REFERENCE/DOCKET NUMBER: 05387.0021-03000

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 408-4000

; TELEFAX: (202) 408-4400

; INFORMATION FOR SEQ ID NO: 122:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-465-325-122

Query Match 27.3%; Score 3; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
|||
Db 7 AKK 9

RESULT 15

US-08-465-325-123

; Sequence 123, Application US/08465325

; Patent No. 5686563

; GENERAL INFORMATION:

; APPLICANT: Magainin Pharmaceuticals Inc.

; APPLICANT: 5110 Campus Drive

; APPLICANT: Plymouth Meeting, PA 19462

; TITLE OF INVENTION: Biologically Active Peptides Having

; TITLE OF INVENTION: N-Terminal Substitutions

; NUMBER OF SEQUENCES: 153

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &

; ADDRESSEE: Dunner

; STREET: 1300 I. Street, N.W. Suite 700

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20005-3315

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/465,325

; FILING DATE: 05-JUN-1995

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/184,462

; FILING DATE: 18-JAN-94

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/891,201

; FILING DATE: 01-JUN-92

; ATTORNEY/AGENT INFORMATION:

; NAME: Fordis, Jean B

; REGISTRATION NUMBER: 32,984

; REFERENCE/DOCKET NUMBER: 05387.0021-03000

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 408-4000

; TELEFAX: (202) 408-4400

; INFORMATION FOR SEQ ID NO: 123:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-465-325-123

Query Match 27.3%; Score 3; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
|||
Db 7 AKK 9

RESULT 16

US-08-411-727-10

; Sequence 10, Application US/08411727

; Patent No. 5705161

; Patent No. 5705161 5683703

; GENERAL INFORMATION:

; APPLICANT: VAN DER LEY, Peter Andre

; APPLICANT: POOLMAN, Jan Theunis

; APPLICANT: HOOGERHOUT, Peter

; TITLE OF INVENTION: IMMUNOGENIC MENINGOCOCCAL LPS AND OTHER

; TITLE OF INVENTION: MEMBRANE VESICLES AND VACCINE THEREFROM

; NUMBER OF SEQUENCES: 30

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: YOUNG & THOMPSON

; STREET: 745 South 23rd Street, Suite 200

; CITY: Arlington

; STATE: Virginia

; COUNTRY: U.S.A.

; ZIP: 22202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/411,727

; FILING DATE: 01-MAY-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: NL 9201716

; FILING DATE: 02-OCT-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/NL93/00163

; FILING DATE: 30-JUL-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: PATCH, Andrew J.

; REGISTRATION NUMBER: 32925

; REFERENCE/DOCKET NUMBER: BO 38275

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-521-2297

; TELEFAX: 703-685-0573

; TELEX: 248425 EMBON

; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-411-727-10

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KDT 10
|||
Db 3 KDT 5

RESULT 17

US-08-411-727-18

; Sequence 18, Application US/08411727
; Patent No. 5705161
; Patent No. 5705161 5683703
; GENERAL INFORMATION:
; APPLICANT: VAN DER LEY, Peter Andre
; APPLICANT: POOLMAN, Jan Theunis
; APPLICANT: HOOGERHOUT, Peter
; TITLE OF INVENTION: IMMUNOGENIC MENINGOCOCCAL LPS AND OTHER
; TITLE OF INVENTION: MEMBRANE VESICLES AND VACCINE THEREFROM
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street, Suite 200
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/411,727
; FILING DATE: 01-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: NL 9201716
; FILING DATE: 02-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/NL93/00163
; FILING DATE: 30-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32925
; REFERENCE/DOCKET NUMBER: BO 38275
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-521-2297
; TELEFAX: 703-685-0573
; TELEX: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-411-727-18

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KDT 10
|||
Db 3 KDT 5

RESULT 18

US-08-548-540-119

; Sequence 119, Application US/08548540
; Patent No. 5733731

; GENERAL INFORMATION:

; APPLICANT: Schatz, Peter J.
; APPLICANT: Cull, Millard G.
; APPLICANT: Miller, Jeff F.
; APPLICANT: Stemmer, Willem P.C.
; APPLICANT: Gates, Christian M.
; TITLE OF INVENTION: Peptide Library and Screening Method
; NUMBER OF SEQUENCES: 162
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/548,540
; FILING DATE: 26-OCT-1995
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/290,641
; FILING DATE: 15-AUG-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/963,321
; FILING DATE: 15-OCT-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 16528J-001240US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422

; INFORMATION FOR SEQ ID NO: 119:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-548-540-119

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ERQ 6
|||
Db 4 ERQ 6

RESULT 19

US-08-530-524A-25

; Sequence 25, Application US/08530524A
; Patent No. 5837836

; GENERAL INFORMATION:

; APPLICANT: Friderici, Karen
; APPLICANT: Jones, Margaret
; APPLICANT: Chen, Hong
; APPLICANT: Cavanagh, Kevin
; TITLE OF INVENTION: Bovine Beta-Mannosidase Gene and Methods
; TITLE OF INVENTION: of Use
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
; STREET: P.O. Box 828
; CITY: Bloomfield Hills
; STATE: Michigan
; COUNTRY: USA
; ZIP: 48303

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/530,524A
; FILING DATE: September 19, 1995
; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: Smith, DeAnn F.
; REGISTRATION NUMBER: 36,683
; REFERENCE/DOCKET NUMBER: 6550-00003DVA

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (810)641-1600
; TELEFAX: (810)641-0270

; INFORMATION FOR SEQ ID NO: 25:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-530-524A-25

Query Match 27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KDT 10
|||
Db 2 KDT 4

RESULT 20

US-08-248-839C-26

; Sequence 26, Application US/08248839C
; Patent No. 5843702

; GENERAL INFORMATION:

; APPLICANT: McConnell, David

; APPLICANT: Devine, Kevin

; APPLICANT: O'Kane, Charles

; TITLE OF INVENTION: A Gene Expression System

; NUMBER OF SEQUENCES: 185

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: No. 5843702o No. 5843702disk of No. 5843702th America, Inc.

; STREET: 405 Lexington Avenue

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10174-6401

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/248,839C

; FILING DATE: 25-MAY-1994

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Gregg, Valeta A.

; REGISTRATION NUMBER: 35,127

; REFERENCE/DOCKET NUMBER: 3614.214-US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-867-0123

; TELEFAX: 212-878-9655

; INFORMATION FOR SEQ ID NO: 26:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: Protein

US-08-248-839C-26

Query Match 27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7
|||
Db 9 RQR 11

RESULT 21
 US-08-636-176-8
 ; Sequence 8, Application US/08636176
 ; Patent No. 5846822
 ; GENERAL INFORMATION:
 ; APPLICANT: Meuer, S.
 ; APPLICANT: Schraven, B.
 ; APPLICANT: Schoenhaut, D.
 ; APPLICANT: Ratnofsky, S.
 ; TITLE OF INVENTION: pp32: A Newly Identified CD45-Associated
 ; TITLE OF INVENTION: Protein
 ; NUMBER OF SEQUENCES: 20
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LAHIVE & COCKFIELD
 ; STREET: 60 STATE STREET, SUITE 510
 ; CITY: BOSTON
 ; STATE: MASSACHUSETTS
 ; COUNTRY: USA
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: ASCII text
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/636,176
 ; FILING DATE:
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/688,019; 08/004,199
 ; FILING DATE: 19-APR-1991; 13-JAN-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: DeConti, Giulio A., Jr.
 ; REGISTRATION NUMBER: 31,503
 ; REFERENCE/DOCKET NUMBER: BBI-006CNCP
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 227-7400
 ; TELEFAX: (617) 227-5941
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 11 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; FRAGMENT TYPE: internal
 US-08-636-176-8

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ERQ 6
 |||
 Db 9 ERQ 11

RESULT 22

US-08-737-085A-12

```
; Sequence 12, Application US/08737085A
; Patent No. 5869232
; GENERAL INFORMATION:
;   APPLICANT: SALLBERG, MATTI
;   TITLE OF INVENTION: ANTIGEN/ANTIBODY SPECIFICITY
;   TITLE OF INVENTION: EXCHANGER
;   NUMBER OF SEQUENCES: 23
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: DARBY & DARBY PC
;     STREET: 805 Third Avenue
;     CITY: New York
;     STATE: New York
;     COUNTRY: USA
;     ZIP: 10022
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Diskette
;     COMPUTER: IBM Compatible
;     OPERATING SYSTEM: DOS
;     SOFTWARE: FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/737,085A
;     FILING DATE: 27-DEC-1996
;     CLASSIFICATION: 426
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:
;     FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Green, Reza
;     REGISTRATION NUMBER: 38,475
;     REFERENCE/DOCKET NUMBER: 3846/0C569
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 212-527-7659
;     TELEFAX: 212-753-6237
;     TELEX: 236687
;   INFORMATION FOR SEQ ID NO: 12:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 11 amino acids
;       TYPE: amino acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;     MOLECULE TYPE: peptide
```

US-08-737-085A-12

```
Query Match          27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy          6 QRK 8
            |||
Db          1 QRK 3
```

RESULT 23

US-08-538-960-8

```

; Sequence 8, Application US/08538960
; Patent No. 5872230
; GENERAL INFORMATION:
;   APPLICANT: Stocco, Douglas M.
;   APPLICANT: Clark, Barbara J.
;   TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
;   TITLE OF INVENTION: REGULATION OF STEROIDOGENESIS
;   NUMBER OF SEQUENCES: 14
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Akin, Gump, Strauss, Hauer & Feld, L.L.P.
;     STREET: 1900 Frost Bank Plaza, 816 Congress Avenue
;     CITY: Austin
;     STATE: TX
;     COUNTRY: U.S.A.
;     ZIP: 78701
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/538,960
;     FILING DATE: Concurrently Herewith
;     CLASSIFICATION: 530
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Mayfield, Denise L.
;     REGISTRATION NUMBER: 33,732
;     REFERENCE/DOCKET NUMBER: 43375.0002/DLM
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 512/499-6200
;     TELEFAX: 512/499-6290
;   INFORMATION FOR SEQ ID NO: 8:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 11 amino acids
;       TYPE: amino acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;     MOLECULE TYPE: peptide
US-08-538-960-8

```

```

Query Match          27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

QY      2 KKE 4
      |||
Db      9 KKE 11

```

RESULT 24

US-08-893-853-54

```

; Sequence 54, Application US/08893853
; Patent No. 5891994
; GENERAL INFORMATION:
;   APPLICANT: Goldstein, Gideon
;   TITLE OF INVENTION: Methods and Compositions for Impairing
;   TITLE OF INVENTION: Multiplication of HIV-1

```

```

; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Cntr., P.O. Box 457
; CITY: Spring House
; STATE: PA
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/893,853
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: GGP2USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9200
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-893-853-54

```

```

Query Match          27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      5 RQR 7
      |||
Db      2 RQR 4

```

```

RESULT 25
US-08-893-853-74
; Sequence 74, Application US/08893853
; Patent No. 5891994
; GENERAL INFORMATION:
; APPLICANT: Goldstein, Gideon
; TITLE OF INVENTION: Methods and Compositions for Impairing
; TITLE OF INVENTION: Multiplication of HIV-1
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Cntr., P.O. Box 457
; CITY: Spring House
; STATE: PA
; COUNTRY: USA

```

```

; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/893,853
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: GGP2USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9200
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 74:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-893-853-74

```

```

Query Match          27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      5 RQR 7
      |||
Db      2 RQR 4

```

RESULT 26

US-08-466-975A-3

```

; Sequence 3, Application US/08466975A
; Patent No. 5910404
; GENERAL INFORMATION:
; APPLICANT: DELEYS, ROBERT J
; APPLICANT: POLLET, DIRK
; APPLICANT: MAERTENS, GEERT
; APPLICANT: VAN HEUVERSWUN, HUGO
; TITLE OF INVENTION: SYNTHETIC ANTIGENS FOR THE DETECTION OF
; TITLE OF INVENTION: ANTIBODIES TO HEPATITIS C VIRUS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

```

```

;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/466,975A
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/391,671
;   FILING DATE:
;   APPLICATION NUMBER:  US 07/920,286
;   FILING DATE:  14-OCT-1992
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  WO PCT/EP91/02409
;   FILING DATE:  13-DEC-1991
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  EP 90124241.2
;   FILING DATE:  14-DEC-1990
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  SADOFF, B.J.
;   REGISTRATION NUMBER:  36,663
;   REFERENCE/DOCKET NUMBER:  1487-5
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  7038164000
;   TELEFAX:  7038164100
;   INFORMATION FOR SEQ ID NO:  3:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  11 amino acids
;   TYPE:  amino acid
;   STRANDEDNESS:  single
;   TOPOLOGY:  linear
;   MOLECULE TYPE:  peptide
US-08-466-975A-3

```

```

Query Match          27.3%;  Score 3;  DB 2;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 2.3e+03;
Matches      3;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy      6 QRK 8
      |||
Db      1 QRK 3

```

RESULT 27

US-08-391-671A-3

```

; Sequence 3, Application US/08391671A
; Patent No. 5922532
;   GENERAL INFORMATION:
;   APPLICANT:  DELEYS, ROBERT J
;   APPLICANT:  POLLET, DIRK
;   APPLICANT:  MAERTENS, GEERT
;   APPLICANT:  VAN HEUVERSWUN, HUGO
;   TITLE OF INVENTION:  SYNTHETIC ANTIGENS FOR THE DETECTION OF
;   TITLE OF INVENTION:  ANTIBODIES TO HEPATITIS C VIRUS
;   NUMBER OF SEQUENCES:  23
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  NIXON & VANDERHYE P.C.
;   STREET:  1100 NORTH GLEBE ROAD

```


; CITY: ARLINGTON
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22201
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/391,671A
 ; FILING DATE: 21-FEB-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/920,286
 ; FILING DATE: 14-OCT-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: WO PCT/EP91/02409
 ; FILING DATE: 13-DEC-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: EP 90124241.2
 ; FILING DATE: 14-DEC-1990
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: SADOFF, B.J.
 ; REGISTRATION NUMBER: 36,663
 ; REFERENCE/DOCKET NUMBER: 1487-5
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 7038164000
 ; TELEFAX: 7038164100
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 11 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-08-391-671A-3

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QRK 8
 |||
 Db 1 QRK 3

RESULT 28
 US-08-789-588-16
 ; Sequence 16, Application US/08789588
 ; Patent No. 5922846
 ; GENERAL INFORMATION:
 ; APPLICANT: Cerletti, Nico
 ; APPLICANT: McMaster, Gary K.
 ; APPLICANT: Cox, David
 ; APPLICANT: Schmitz, Albert
 ; APPLICANT: Meyhack, Bernd

```

; TITLE OF INVENTION: Process for Refolding Recombinantly
; TITLE OF INVENTION: Produced TGF-beta-like Proteins
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Henry P. No. 5922846ak
; STREET: 520 White Plains Road, P.O. Box 2005
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-9005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/789,588
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/486,057
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/201,703
; FILING DATE: 25-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/960,309
; FILING DATE: 13-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/621,502
; FILING DATE: 03-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8927546.5
; FILING DATE: 06-DEC-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5922846ak, Henry P.
; REGISTRATION NUMBER: 33200
; REFERENCE/DOCKET NUMBER: 4-17861/+ /Cont3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 277-5110
; TELEFAX: (908) 277-4306
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-789-588-16

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Query Match          27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      9 DTQ 11
        |||
Db      1 DTQ 3

```

RESULT 29

US-08-760-075A-1

```
; Sequence 1, Application US/08760075A
; Patent No. 5942429
; GENERAL INFORMATION:
;   APPLICANT: KIRSCHBAUM, Bernd
;   APPLICANT: MUELLNER, Stefan
;   APPLICANT: BARTLETT, Robert
;   TITLE OF INVENTION: NOVEL DEAH-BOX PROTEINS
;   NUMBER OF SEQUENCES: 38
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Foley & Lardner
;     STREET: 3000 K Street, N.W., Suite 500
;     CITY: Washington
;     STATE: D.C.
;     COUNTRY: USA
;     ZIP: 20007-5109
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/760,075A
;     FILING DATE: 04-DEC-1996
;     CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: DE 19545126.0
;     FILING DATE: 04-DEC-1995
;   ATTORNEY/AGENT INFORMATION:
;     NAME: GRANADOS, Patricia D.
;     REGISTRATION NUMBER: 33,683
;     REFERENCE/DOCKET NUMBER: 18748/309
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (202)672-5300
;     TELEFAX: (202)672-5399
;     TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 11 amino acids
;       TYPE: amino acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
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US-08-760-075A-1

```
Query Match          27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy          2 KKE 4
            |||
Db          9 KKE 11
```

RESULT 30

US-08-706-741B-54

```

; Sequence 54, Application US/08706741B
; Patent No. 5955593
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, STANLEY J.
; TITLE OF INVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 63146
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/706,741B
; FILING DATE: 09-SEP-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 965017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-706-741B-54

```

```

Query Match          27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      5 RQR 7
      |||
Db      7 RQR 9

```

RESULT 31

```

US-08-924-695A-54
; Sequence 54, Application US/08924695A
; Patent No. 5998583
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, STANLEY J.
; TITLE OF INVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.

```

; STREET: 7733 FORSYTH BLVD., SUITE 1400
 ; CITY: ST. LOUIS
 ; STATE: MISSOURI
 ; COUNTRY: USA
 ; ZIP: 63105
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/924,695A
 ; FILING DATE: 09-SEP-1997
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: HOLLAND, DONALD R.
 ; REGISTRATION NUMBER: 35,197
 ; REFERENCE/DOCKET NUMBER: 971798
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (314) 727-5188
 ; TELEFAX: (314) 727-6092
 ; INFORMATION FOR SEQ ID NO: 54:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 11 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-08-924-695A-54

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7
 |||
 Db 7 RQR 9

RESULT 32

US-08-467-902A-3

; Sequence 3, Application US/08467902A
 ; Patent No. 6007982
 ; GENERAL INFORMATION:
 ; APPLICANT: DELEYS, ROBERT J
 ; APPLICANT: POLLET, DIRK
 ; APPLICANT: MAERTENS, GEERT
 ; APPLICANT: VAN HEUVERSWUN, HUGO
 ; TITLE OF INVENTION: SYNTHETIC ANTIGENS FOR THE DETECTION OF
 ; TITLE OF INVENTION: ANTIBODIES TO HEPATITIS C VIRUS
 ; NUMBER OF SEQUENCES: 23
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: NIXON & VANDERHYE P.C.
 ; STREET: 1100 NORTH GLEBE ROAD
 ; CITY: ARLINGTON
 ; STATE: VA
 ; COUNTRY: USA

```

; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,902A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/391,671
; FILING DATE:
; APPLICATION NUMBER: US 07/920,286
; FILING DATE: 14-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP91/02409
; FILING DATE: 13-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 90124241.2
; FILING DATE: 14-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 1487-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 7038164000
; TELEFAX: 7038164100
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-467-902A-3

```

```

Query Match          27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      6 QRK 8
      |||
Db      1 QRK 3

```

```

RESULT 33
US-09-246-258-12
; Sequence 12, Application US/09246258
; Patent No. 6040137
; GENERAL INFORMATION:
; APPLICANT: SALLBERG, MATTI
; TITLE OF INVENTION: ANTIGEN/ANTIBODY SPECIFICITY
; TITLE OF INVENTION: EXCHANGER
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DARBY & DARBY PC

```

```

; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/246,258
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/737,085
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475
; REFERENCE/DOCKET NUMBER: 3846/OC569
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7659
; TELEFAX: 212-753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-246-258-12

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```

Query Match          27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy      6 QRK 8
        |||
Db      1 QRK 3

```

```

RESULT 34
US-09-188-579-65
; Sequence 65, Application US/09188579B
; Patent No. 6107040
; GENERAL INFORMATION:
; APPLICANT: Shuman, Stewart
; TITLE OF INVENTION: Pharmacological Targeting of mRNA Cap Formation
; FILE REFERENCE: D6185
; CURRENT APPLICATION NUMBER: US/09/188,579B
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 114
; SEQ ID NO 65
; LENGTH: 11
; TYPE: PRT

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; ORGANISM: vaccinia virus
; FEATURE:
; OTHER INFORMATION: Motif V of RNA guanylyltransferase.
US-09-188-579-65

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKE 4
|||
Db 5 KKE 7

RESULT 35

US-08-602-999A-284

; Sequence 284, Application US/08602999A

; Patent No. 6184205

; GENERAL INFORMATION:

; APPLICANT: SPARKS, Andrew B.

; APPLICANT: KAY, Brian K.

; APPLICANT: THORN, Judith M.

; APPLICANT: QUILLIAM, Lawrence A.

; APPLICANT: DER, Channing J.

; APPLICANT: FOWLKES, Dana M.

; APPLICANT: RIDER, James E.

; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF

; TITLE OF INVENTION: ISOLATING AND USING SAME

; NUMBER OF SEQUENCES: 467

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/602,999A

; FILING DATE: 16-FEB-1996

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Misrock, S. Leslie

; REGISTRATION NUMBER: 18,872

; REFERENCE/DOCKET NUMBER: 1101-202

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090

; TELEFAX: (212) 869-9741/8864

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 284:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-284

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KER 5
|||
Db 9 KER 11

RESULT 36

US-09-113-921-74

; Sequence 74, Application US/09113921

; Patent No. 6193981

; GENERAL INFORMATION:

; APPLICANT: Goldstein, Gideon

; TITLE OF INVENTION: Methods and Compositions for Impairing

; TITLE OF INVENTION: Multiplication of HIV-1

; NUMBER OF SEQUENCES: 124

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Howson and Howson

; STREET: Spring House Corporate Cntr., P.O. Box 457

; CITY: Spring House

; STATE: PA

; COUNTRY: USA

; ZIP: 19477

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/113,921

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/893,853

; FILING DATE: 11-JUL-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Bak, Mary E.

; REGISTRATION NUMBER: 31,215

; REFERENCE/DOCKET NUMBER: GGP2AUSA

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 215-540-9200

; TELEFAX: 215-540-5818

; INFORMATION FOR SEQ ID NO: 74:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-09-113-921-74

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7
|||
Db 2 RQR 4

RESULT 37

US-08-659-254-8

; Sequence 8, Application US/08659254
; Patent No. 6194555
; GENERAL INFORMATION:
; APPLICANT: Stocco, Douglas M.
; APPLICANT: Clark, Dr. Barbara J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATION
; TITLE OF INVENTION: OF STEROIDOGENESIS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Akin, Gump, Strauss, Hauer & Feld, L.L.P.
; STREET: 1900 Frost Bank Plaza, 816 Congress Avenue
; CITY: Austin
; STATE: TX
; COUNTRY: U.S.A.
; ZIP: 78701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/659,254
; FILING DATE: 07-JUN-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/538,960
; FILING DATE: 04-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Mayfield, Denise L.
; REGISTRATION NUMBER: 33,732
; REFERENCE/DOCKET NUMBER: 43375.0006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/499-6200
; TELEFAX: 512/499-6290
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-659-254-8

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKE 4
|||
Db 9 KKE 11

RESULT 38

US-09-206-059-23

; Sequence 23, Application US/09206059
; Patent No. 6201104
; GENERAL INFORMATION:
; APPLICANT: MacDonald, Nicholas
; APPLICANT: Sim, Kim Lee
; TITLE OF INVENTION: Angiogenesis-Inhibiting Protein Binding Peptides and
; TITLE OF INVENTION: Proteins and Methods of Use
; FILE REFERENCE: 05213-0370
; CURRENT APPLICATION NUMBER: US/09/206,059
; CURRENT FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: binding peptides
US-09-206-059-23

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RKD 9
|||
Db 5 RKD 7

RESULT 39

US-09-208-966-2

; Sequence 2, Application US/09208966
; Patent No. 6221355
; GENERAL INFORMATION:
; APPLICANT: Dowdy, Steven F.
; TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF
; FILE REFERENCE: 48881/1742
; CURRENT APPLICATION NUMBER: US/09/208,966
; CURRENT FILING DATE: 1998-12-10
; EARLIER APPLICATION NUMBER: 60/082,402
; EARLIER FILING DATE: 1998-04-20
; EARLIER APPLICATION NUMBER: 60/069,012
; EARLIER FILING DATE: 1997-12-10
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 11
; TYPE: PRT

; ORGANISM: human
US-09-208-966-2

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7
|||
Db 7 RQR 9

RESULT 40

US-09-208-966-16

; Sequence 16, Application US/09208966

; Patent No. 6221355

; GENERAL INFORMATION:

; APPLICANT: Dowdy, Steven F.

; TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF

; FILE REFERENCE: 48881/1742

; CURRENT APPLICATION NUMBER: US/09/208,966

; CURRENT FILING DATE: 1998-12-10

; EARLIER APPLICATION NUMBER: 60/082,402

; EARLIER FILING DATE: 1998-04-20

; EARLIER APPLICATION NUMBER: 60/069,012

; EARLIER FILING DATE: 1997-12-10

; NUMBER OF SEQ ID NOS: 57

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 16

; LENGTH: 11

; TYPE: PRT

; ORGANISM: human

US-09-208-966-16

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7
|||
Db 6 RQR 8

RESULT 41

US-09-208-966-52

; Sequence 52, Application US/09208966

; Patent No. 6221355

; GENERAL INFORMATION:

; APPLICANT: Dowdy, Steven F.

; TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF

; FILE REFERENCE: 48881/1742

; CURRENT APPLICATION NUMBER: US/09/208,966

; CURRENT FILING DATE: 1998-12-10

; EARLIER APPLICATION NUMBER: 60/082,402

; EARLIER FILING DATE: 1998-04-20

; EARLIER APPLICATION NUMBER: 60/069,012

; EARLIER FILING DATE: 1997-12-10

; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 52
; LENGTH: 11
; TYPE: PRT
; ORGANISM: human
US-09-208-966-52

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7
|||
Db 7 RQR 9

RESULT 42

US-08-647-405B-6
; Sequence 6, Application US/08647405B
; Patent No. 6228654
; GENERAL INFORMATION:
; APPLICANT: Chait, Brian T.
; APPLICANT: Zhao, Yingming
; APPLICANT: Kent, Stephen B.H.
; TITLE OF INVENTION: METHODS FOR STRUCTURE ANALYSIS OF OLIGOSACCHARIDES
; FILE REFERENCE: Oligosaccharides
; CURRENT APPLICATION NUMBER: US/08/647,405B
; CURRENT FILING DATE: 1996-05-09
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Related to
; OTHER INFORMATION: human translationally controlled tumor protein
US-08-647-405B-6

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KDT 10
|||
Db 4 KDT 6

RESULT 43

US-09-177-249-204
; Sequence 204, Application US/09177249
; Patent No. 6229064
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Ohad, Nir
; APPLICANT: Kiyosue, Tomohiro

```
; APPLICANT: Yadegari, Ramin
; APPLICANT: Margossian, Linda
; APPLICANT: Harada, John
; APPLICANT: Goldberg, Robert B.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit
; TITLE OF INVENTION: Development in Plants
; FILE REFERENCE: 023070-086120US
; CURRENT APPLICATION NUMBER: US/09/177,249
; CURRENT FILING DATE: 1998-10-22
; EARLIER APPLICATION NUMBER: US 09/071,838
; EARLIER FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 204
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Arabidopsis sp.
US-09-177-249-204
```

```
Query Match          27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative    0; Mismatches    0; Indels      0; Gaps      0;
```

```
Qy          7 RKD 9
             |||
Db          3 RKD 5
```

RESULT 44

```
US-09-315-444-65
; Sequence 65, Application US/09315444A
; Patent No. 6232070
; GENERAL INFORMATION:
; APPLICANT: Shuman, Stewart
; TITLE OF INVENTION: Pharmacological Targeting of mRNA Cap Formation
; FILE REFERENCE: D6185CIP
; CURRENT APPLICATION NUMBER: US/09/315,444A
; CURRENT FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: US 09/188,579
; PRIOR FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 65
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: vaccinia virus
;   FEATURE:
;   OTHER INFORMATION: Motif V of RNA guanylyltransferase.
US-09-315-444-65
```

```
Query Match          27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative    0; Mismatches    0; Indels      0; Gaps      0;
```

```
Qy          2 KKE 4
             |||
Db          5 KKE 7
```

RESULT 45

US-09-532-106-12

; Sequence 12, Application US/09532106

; Patent No. 6245895

; GENERAL INFORMATION:

; APPLICANT: SALLBERG, MATTI

; TITLE OF INVENTION: ANTIGEN/ANTIBODY SPECIFICITY
EXCHANGER

; NUMBER OF SEQUENCES: 23

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DARBY & DARBY PC

; STREET: 805 Third Avenue

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10022

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/532,106

; FILING DATE: 21-Mar-2000

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/737,085A

; FILING DATE: 27-DEC-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Green, Reza

; REGISTRATION NUMBER: 38,475

; REFERENCE/DOCKET NUMBER: 3846/0C569

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-527-7659

; TELEFAX: 212-753-6237

; TELEX: 236687

; INFORMATION FOR SEQ ID NO: 12:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 12:

US-09-532-106-12

Query Match 27.3%; Score 3; DB 3; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QRK 8

|||

Db 1 QRK 3

RESULT 46

US-09-338-546-1
; Sequence 1, Application US/09338546
; Patent No. 6251645
; GENERAL INFORMATION:
; APPLICANT: KIRSCHBAUM, Bernd
; APPLICANT: MUELLNER, Stefan
; APPLICANT: BARTLETT, Robert
; TITLE OF INVENTION: NOVEL DEAH-BOX PROTEINS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/338,546
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/760,075
; FILING DATE: 04-DEC-1996
; APPLICATION NUMBER: DE 19545126.0
; FILING DATE: 04-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 18748/309
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-09-338-546-1

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKE 4
|||
Db 9 KKE 11

RESULT 47
US-09-142-732-6


```

; Sequence 6, Application US/09142732
; Patent No. 6252045
; GENERAL INFORMATION:
;   APPLICANT: James M. Anderson
;   APPLICANT: Christina M. Van Itallie
;   TITLE OF INVENTION: Human Occludin, Its Uses and
;   TITLE OF INVENTION: Enhancement of Drug Absorption Using Occludin
Inhibitors
;   NUMBER OF SEQUENCES: 6
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Yale University Medical School
;     ADDRESSEE: Section of Digestive Diseases
;     ADDRESSEE: Department of Internal Medicine
;     STREET: 333 Cedar Street, LCI 105
;     CITY: New Haven
;     STATE: Connecticut
;     COUNTRY: United States of America
;     ZIP: 06520-8057
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: 3.5" 1.44 Mb diskette
;     COMPUTER: IBM PC
;     OPERATING SYSTEM: MS DOS
;     SOFTWARE: Word Processing
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/142,732
;     FILING DATE:
;     CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: PCT/US97/05809
;     FILING DATE: March 14, 1997
;     APPLICATION NUMBER: U.S. 60/013,625
;     FILING DATE: March 15, 1996
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Mary M. Krinsky
;     REGISTRATION NUMBER: 32423
;     REFERENCE/DOCKET NUMBER: 1751-P0016B.PCT
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 203-324-6155
;     TELEFAX: 203-327-1096
;   INFORMATION FOR SEQ ID NO: 6:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 11
;       TYPE: amino acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;     MOLECULE TYPE:
;       DESCRIPTION: peptide
;     FRAGMENT TYPE: synthetic peptide
;     FEATURE:
;       OTHER INFORMATION: construct used in experi-
;       OTHER INFORMATION: ments
US-09-142-732-6

```

```

Query Match          27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

Qy 7 RKD 9
| | |
Db 7 RKD 9

RESULT 48

US-09-044-411-1
; Sequence 1, Application US/09044411A
; Patent No. 6258774
; GENERAL INFORMATION:
; APPLICANT: Stein, Stanley
; TITLE OF INVENTION: CARRIER FOR IN VIVO DELIVERY OF A THERAPEUTIC
; FILE REFERENCE: 601-1-083
; CURRENT APPLICATION NUMBER: US/09/044,411A
; CURRENT FILING DATE: 1998-03-19
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; FEATURE:
; OTHER INFORMATION: Internal sequence from the Tat protein, but with
; OTHER INFORMATION: an extra Cys not found in natural protein.
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (10)
; OTHER INFORMATION: Xaa is either Cys(biotin) or Lys(biotin) at this
; OTHER INFORMATION: position.
; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (10)
; OTHER INFORMATION: Either Cys(biotin) or Lys(biotin) at this
; OTHER INFORMATION: position.
; FEATURE:
; OTHER INFORMATION: Peptide has an N-terminal carboxylic acid residue.
; FEATURE:
; OTHER INFORMATION: Peptide has a C-terminal amide group.
US-09-044-411-1

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7
| | |
Db 5 RQR 7

RESULT 49

US-09-044-411-2
; Sequence 2, Application US/09044411A
; Patent No. 6258774
; GENERAL INFORMATION:
; APPLICANT: Stein, Stanley
; TITLE OF INVENTION: CARRIER FOR IN VIVO DELIVERY OF A THERAPEUTIC
; FILE REFERENCE: 601-1-083

```

; CURRENT APPLICATION NUMBER: US/09/044,411A
; CURRENT FILING DATE: 1998-03-19
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; FEATURE:
; OTHER INFORMATION: Internal sequence from the Tat protein, but with
; OTHER INFORMATION: two extra Cys residues not found in thenatural
; OTHER INFORMATION: protein.
; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (10)
; OTHER INFORMATION: Cys(biotin)
; FEATURE:
; OTHER INFORMATION: Peptide has an N-terminal acetyl group.
; FEATURE:
; OTHER INFORMATION: Peptide has a C-terminal amide group.
US-09-044-411-2

```

```

Query Match          27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      5 RQR 7
      |||
Db      5 RQR 7

```

RESULT 50

```

US-09-044-411-3
; Sequence 3, Application US/09044411A
; Patent No. 6258774
; GENERAL INFORMATION:
; APPLICANT: Stein, Stanley
; TITLE OF INVENTION: CARRIER FOR IN VIVO DELIVERY OF A THERAPEUTIC
; FILE REFERENCE: 601-1-083
; CURRENT APPLICATION NUMBER: US/09/044,411A
; CURRENT FILING DATE: 1998-03-19
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; FEATURE:
; OTHER INFORMATION: Internal sequence from the Tat protein, but with
; OTHER INFORMATION: an extra Lys and an extra Cys not found in the
; OTHER INFORMATION: natural protein.
; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (10)
; OTHER INFORMATION: Lys(biotin)
; FEATURE:
; OTHER INFORMATION: Peptide has an N-terminal acetyl group.

```

; FEATURE:
; OTHER INFORMATION: Peptide has a C-terminal amide group.
US-09-044-411-3

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7
|||
Db 5 RQR 7

RESULT 51

US-09-044-411-4

; Sequence 4, Application US/09044411A
; Patent No. 6258774
; GENERAL INFORMATION:
; APPLICANT: Stein, Stanley
; TITLE OF INVENTION: CARRIER FOR IN VIVO DELIVERY OF A THERAPEUTIC
; FILE REFERENCE: 601-1-083
; CURRENT APPLICATION NUMBER: US/09/044,411A
; CURRENT FILING DATE: 1998-03-19
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; FEATURE:
; OTHER INFORMATION: Internal sequence from the Tat protein, but with
; OTHER INFORMATION: two extra Cys not found in the natural protein.
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (10)
; OTHER INFORMATION: Cys is the D isomer at this position.
; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (10)
; OTHER INFORMATION: D-Cys(biotin)
; FEATURE:
; OTHER INFORMATION: Peptide has an N-terminal acetyl group.
; FEATURE:
; OTHER INFORMATION: Peptide has a C-terminal amide group.
US-09-044-411-4

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7
|||
Db 5 RQR 7

RESULT 52

US-09-044-411-5

```

; Sequence 5, Application US/09044411A
; Patent No. 6258774
; GENERAL INFORMATION:
; APPLICANT: Stein, Stanley
; TITLE OF INVENTION: CARRIER FOR IN VIVO DELIVERY OF A THERAPEUTIC
; FILE REFERENCE: 601-1-083
; CURRENT APPLICATION NUMBER: US/09/044,411A
; CURRENT FILING DATE: 1998-03-19
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Human immunodeficiency virus type 1
;   FEATURE:
;   OTHER INFORMATION: Internal sequence from the Tat protein, but with
;   OTHER INFORMATION: an extra Lys and an extra Cys not found in the
;   OTHER INFORMATION: natural protein.
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (10)
;   OTHER INFORMATION: Lys is D isomer at this position.
;   FEATURE:
;   NAME/KEY: BINDING
;   LOCATION: (10)
;   OTHER INFORMATION: D-Lys(biotin)
;   FEATURE:
;   OTHER INFORMATION: Peptide has an N-terminal acetyl group.
;   FEATURE:
;   OTHER INFORMATION: Peptide has a C-terminal amide group.
US-09-044-411-5

```

```

Query Match          27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      5 RQR 7
      |||
Db      5 RQR 7

```

RESULT 53

```

US-09-044-411-6
; Sequence 6, Application US/09044411A
; Patent No. 6258774
; GENERAL INFORMATION:
; APPLICANT: Stein, Stanley
; TITLE OF INVENTION: CARRIER FOR IN VIVO DELIVERY OF A THERAPEUTIC
; FILE REFERENCE: 601-1-083
; CURRENT APPLICATION NUMBER: US/09/044,411A
; CURRENT FILING DATE: 1998-03-19
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Human immunodeficiency virus type 1

```

```

; FEATURE:
; OTHER INFORMATION: Same as Sequence ID 3, but with a substitution of
; Patent No. 6258774
; OTHER INFORMATION: Arg to Gln.
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (10)
; OTHER INFORMATION: Lys is the D isomer at this position.
; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (10)
; OTHER INFORMATION: D-Lys(biotin)
; FEATURE:
; OTHER INFORMATION: Peptide has an N-terminal acetyl group.
; FEATURE:
; OTHER INFORMATION: Peptide has a C-terminal amide group.
US-09-044-411-6

```

```

Query Match          27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      5 RQR 7
      |||
Db      5 RQR 7

```

RESULT 54

```

US-09-044-411-8
; Sequence 8, Application US/09044411A
; Patent No. 6258774
; GENERAL INFORMATION:
; APPLICANT: Stein, Stanley
; TITLE OF INVENTION: CARRIER FOR IN VIVO DELIVERY OF A THERAPEUTIC
; FILE REFERENCE: 601-1-083
; CURRENT APPLICATION NUMBER: US/09/044,411A
; CURRENT FILING DATE: 1998-03-19
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; FEATURE:
; OTHER INFORMATION: All amino acids in this sequence are D amino acid.
; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (2)
; OTHER INFORMATION: D-Lys(biotin)
; FEATURE:
; OTHER INFORMATION: Peptide has an N-terminal acetyl group.
; FEATURE:
; OTHER INFORMATION: Peptide has a C-terminal amide group.
US-09-044-411-8

```

```

Query Match          27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;

```

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7

|||

Db 5 RQR 7

RESULT 55

US-09-133-062D-28

; Sequence 28, Application US/09133062D

; Patent No. 6258776

; GENERAL INFORMATION:

; APPLICANT: Hemmings, Brian A

; APPLICANT: Millward, Thomas A

; TITLE OF INVENTION: Calcium Regulated Kinase

; FILE REFERENCE: 30110

; CURRENT APPLICATION NUMBER: US/09/133,062D

; CURRENT FILING DATE: 1998-08-12

; PRIOR APPLICATION NUMBER: GB 9717089.8

; PRIOR FILING DATE: 1997-08-12

; PRIOR APPLICATION NUMBER: GB 9717499.9

; PRIOR FILING DATE: 1998-08-19

; NUMBER OF SEQ ID NOS: 34

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 28

; LENGTH: 11

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:synthetic peptide

; OTHER INFORMATION: internal peptide

US-09-133-062D-28

Query Match 27.3%; Score 3; DB 3; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3

|||

Db 3 AKK 5

RESULT 56

US-09-133-062D-29

; Sequence 29, Application US/09133062D

; Patent No. 6258776

; GENERAL INFORMATION:

; APPLICANT: Hemmings, Brian A

; APPLICANT: Millward, Thomas A

; TITLE OF INVENTION: Calcium Regulated Kinase

; FILE REFERENCE: 30110

; CURRENT APPLICATION NUMBER: US/09/133,062D

; CURRENT FILING DATE: 1998-08-12

; PRIOR APPLICATION NUMBER: GB 9717089.8

; PRIOR FILING DATE: 1997-08-12

; PRIOR APPLICATION NUMBER: GB 9717499.9

; PRIOR FILING DATE: 1998-08-19

; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:synthetic peptide
; OTHER INFORMATION: internal peptide
US-09-133-062D-29

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
|||
Db 3 AKK 5

RESULT 57

US-09-275-265-3

; Sequence 3, Application US/09275265
; Patent No. 6287761
; GENERAL INFORMATION:
; APPLICANT: DELEYS, ROBERT J
; APPLICANT: POLLET, DIRK
; APPLICANT: MAERTENS, GEERT
; APPLICANT: VAN HEUVERSWUN, HUGO
; TITLE OF INVENTION: SYNTHETIC ANTIGENS FOR THE DETECTION OF
; TITLE OF INVENTION: ANTIBODIES TO HEPATITIS C VIRUS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/275,265
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/391,671
; FILING DATE: 21-FEB-1995
; APPLICATION NUMBER: US 07/920,286
; FILING DATE: 14-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP91/02409
; FILING DATE: 13-DEC-1991
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP 90124241.2
; FILING DATE: 14-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 1487-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 7038164000
; TELEFAX: 7038164100
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-275-265-3

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QRK 8
|||
Db 1 QRK 3

RESULT 58

US-09-057-897-8

; Sequence 8, Application US/09057897
; Patent No. 6300476
; GENERAL INFORMATION:
; APPLICANT: Lu, Anthony Y.H.
; APPLICANT: Wang, Regina W.
; TITLE OF INVENTION: Anti-Peptide Antibody Against Human
; TITLE OF INVENTION: Cytochrome P450 3A4
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000
; CITY: Rahway
; STATE: NJ
; COUNTRY: US
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/057,897
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hand, J. Mark
; REGISTRATION NUMBER: 36,545
; REFERENCE/DOCKET NUMBER: 19902

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (732)594-3905
; TELEFAX: (732)594-4720
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-057-897-8

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 DTQ 11
|||
Db 7 DTQ 9

RESULT 59

US-09-057-897-13

; Sequence 13, Application US/09057897
; Patent No. 6300476
; GENERAL INFORMATION:
; APPLICANT: Lu, Anthony Y.H.
; APPLICANT: Wang, Regina W.
; TITLE OF INVENTION: Anti-Peptide Antibody Against Human
; TITLE OF INVENTION: Cytochrome P450 3A4
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000
; CITY: Rahway
; STATE: NJ
; COUNTRY: US
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/057,897
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hand, J. Mark
; REGISTRATION NUMBER: 36,545
; REFERENCE/DOCKET NUMBER: 19902
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (732)594-3905
; TELEFAX: (732)594-4720
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids

; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-057-897-13

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 DTQ 11
|||
Db 4 DTQ 6

RESULT 60

US-09-057-897-18

; Sequence 18, Application US/09057897
; Patent No. 6300476
; GENERAL INFORMATION:
; APPLICANT: Lu, Anthony Y.H.
; APPLICANT: Wang, Regina W.
; TITLE OF INVENTION: Anti-Peptide Antibody Against Human
; TITLE OF INVENTION: Cytochrome P450 3A4
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000
; CITY: Rahway
; STATE: NJ
; COUNTRY: US
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/057,897
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hand, J. Mark
; REGISTRATION NUMBER: 36,545
; REFERENCE/DOCKET NUMBER: 19902
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (732)594-3905
; TELEFAX: (732)594-4720
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-057-897-18

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 DTQ 11
|||
Db 1 DTQ 3

RESULT 61

US-09-296-089-37

; Sequence 37, Application US/09296089
; Patent No. 6303576
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Byers, Stephen
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; TITLE OF INVENTION: BETA-CATENIN MEDIATED GENE EXPRESSION
; FILE REFERENCE: 100086.411
; CURRENT APPLICATION NUMBER: US/09/296,089
; CURRENT FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 37
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-09-296-089-37

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7
|||
Db 7 RQR 9

RESULT 62

US-09-025-596-34

; Sequence 34, Application US/09025596
; Patent No. 6340463
; GENERAL INFORMATION:
; APPLICANT: Mitchell, William M.
; APPLICANT: Stratton, Charles W.
; TITLE OF INVENTION: IDENTIFICATION OF ANTIGENIC PEPTIDE
; TITLE OF INVENTION: SEQUENCES
; FILE REFERENCE: VDB98-01
; CURRENT APPLICATION NUMBER: US/09/025,596
; CURRENT FILING DATE: 1998-02-18
; EARLIER APPLICATION NUMBER: 08/911,593
; EARLIER FILING DATE: 1997-08-14
; EARLIER APPLICATION NUMBER: 60/023,921
; EARLIER FILING DATE: 1996-08-14
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 34
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-025-596-34

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
|||
Db 3 AKK 5

RESULT 63

US-09-115-737-111

; Sequence 111, Application US/09115737

; Patent No. 6348445

; GENERAL INFORMATION:

; APPLICANT: U. Prasad Kari
; Taffy J. Williams
; Michael McLane

; TITLE OF INVENTION: Biologically Active Peptides With Reduced
; Toxicity in Animals and a Method for Preparing Same

; NUMBER OF SEQUENCES: 156

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; Dunner, L.L.P.

; STREET: 1300 I Street, N.W. Suite 700

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20005-3315

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.3

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/115,737

; FILING DATE: 15-Jul-1998

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/465,330

; FILING DATE: 05-JUN-1995

; APPLICATION NUMBER: 08/184,462

; FILING DATE: 18-JAN-94

; APPLICATION NUMBER: 07/891,201

; FILING DATE: 01-JUN-92

; ATTORNEY/AGENT INFORMATION:

; NAME: Fordis, Jean B

; REGISTRATION NUMBER: 32,984

; REFERENCE/DOCKET NUMBER: 05387.0021-06000

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 408-4000

; TELEFAX: (202) 408-4400

; INFORMATION FOR SEQ ID NO: 111:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 111:
US-09-115-737-111

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
|||
Db 1 AKK 3

RESULT 64

US-09-115-737-122

; Sequence 122, Application US/09115737

; Patent No. 6348445

; GENERAL INFORMATION:

; APPLICANT: U. Prasad Kari

; Taffy J. Williams

; Michael McLane

; TITLE OF INVENTION: Biologically Active Peptides With Reduced
; Toxicity in Animals and a Method for Preparing Same

; NUMBER OF SEQUENCES: 156

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; Dunner, L.L.P.

; STREET: 1300 I Street, N.W. Suite 700

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20005-3315

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.3

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/115,737

; FILING DATE: 15-Jul-1998

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/465,330

; FILING DATE: 05-JUN-1995

; APPLICATION NUMBER: 08/184,462

; FILING DATE: 18-JAN-94

; APPLICATION NUMBER: 07/891,201

; FILING DATE: 01-JUN-92

; ATTORNEY/AGENT INFORMATION:

; NAME: Fordis, Jean B

; REGISTRATION NUMBER: 32,984

; REFERENCE/DOCKET NUMBER: 05387.0021-06000
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 122:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 122:
US-09-115-737-122

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
| | |
Db 7 AKK 9

RESULT 65

US-09-115-737-123

; Sequence 123, Application US/09115737
; Patent No. 6348445

; GENERAL INFORMATION:

; APPLICANT: U. Prasad Kari
; Taffy J. Williams
; Michael McLane

; TITLE OF INVENTION: Biologically Active Peptides With Reduced
; Toxicity in Animals and a Method for Preparing Same

; NUMBER OF SEQUENCES: 156

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; Dunner, L.L.P.

; STREET: 1300 I Street, N.W. Suite 700

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20005-3315

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.3

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/115,737

; FILING DATE: 15-Jul-1998

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/465,330

; FILING DATE: 05-JUN-1995

; APPLICATION NUMBER: 08/184,462

; FILING DATE: 18-JAN-94

; APPLICATION NUMBER: 07/891,201

```

;          FILING DATE: 01-JUN-92
;    ATTORNEY/AGENT INFORMATION:
;          NAME: Fordis, Jean B
;          REGISTRATION NUMBER: 32,984
;          REFERENCE/DOCKET NUMBER: 05387.0021-06000
;    TELECOMMUNICATION INFORMATION:
;          TELEPHONE: (202) 408-4000
;          TELEFAX: (202) 408-4400
;    INFORMATION FOR SEQ ID NO: 123:
;      SEQUENCE CHARACTERISTICS:
;        LENGTH: 11 amino acids
;        TYPE: amino acid
;        STRANDEDNESS: single
;        TOPOLOGY: linear
;      MOLECULE TYPE: peptide
;      SEQUENCE DESCRIPTION: SEQ ID NO: 123:
US-09-115-737-123

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Query Match          27.3%;  Score 3;  DB 4;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 2.3e+03;
Matches      3;  Conservative    0;  Mismatches    0;  Indels      0;  Gaps      0;

```

```

Qy          1 AKK 3
            |||
Db          7 AKK 9

```

RESULT 66

```

US-09-187-859-3110
; Sequence 3110, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C1
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3110
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Representative cyclic modulating agent based on
;   OTHER INFORMATION: Desmoglein cell adhesion recognition sequence
US-09-187-859-3110

```

```

Query Match          27.3%;  Score 3;  DB 4;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 2.3e+03;
Matches      3;  Conservative    0;  Mismatches    0;  Indels      0;  Gaps      0;

```

```

Qy          8 KDT 10
            |||
Db          7 KDT 9

```


RESULT 67

US-09-187-859-3155

; Sequence 3155, Application US/09187859A
 ; Patent No. 6358920
 ; GENERAL INFORMATION:
 ; APPLICANT: Blaschuk, Orest W.
 ; APPLICANT: Gour, Barbara J.
 ; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
 ; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
 ; FILE REFERENCE: 100086.407C1
 ; CURRENT APPLICATION NUMBER: US/09/187,859A
 ; CURRENT FILING DATE: 1998-11-06
 ; NUMBER OF SEQ ID NOS: 4052
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 3155
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Representative cyclic modulating agent based on
 ; OTHER INFORMATION: Desmoglein cell adhesion recognition sequence

US-09-187-859-3155

Query Match 27.3%; Score 3; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KDT 10
 |||
 Db 7 KDT 9

RESULT 68

US-09-187-859-3200

; Sequence 3200, Application US/09187859A
 ; Patent No. 6358920
 ; GENERAL INFORMATION:
 ; APPLICANT: Blaschuk, Orest W.
 ; APPLICANT: Gour, Barbara J.
 ; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
 ; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
 ; FILE REFERENCE: 100086.407C1
 ; CURRENT APPLICATION NUMBER: US/09/187,859A
 ; CURRENT FILING DATE: 1998-11-06
 ; NUMBER OF SEQ ID NOS: 4052
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 3200
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Representative cyclic modulating agent based on
 ; OTHER INFORMATION: Desmoglein cell adhesion recognition sequence

US-09-187-859-3200

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KDT 10
|||
Db 7 KDT 9

RESULT 69

US-09-187-859-3245
; Sequence 3245, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C1
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3245
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: Desmoglein cell adhesion recognition sequence
US-09-187-859-3245

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KDT 10
|||
Db 7 KDT 9

RESULT 70

US-09-187-859-3290
; Sequence 3290, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C1
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3290
; LENGTH: 11

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: Desmoglein cell adhesion recognition sequence
US-09-187-859-3290

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KDT 10
|||
Db 7 KDT 9

RESULT 71

US-09-187-859-3341
; Sequence 3341, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C1
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3341
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: Desmocollin cell adhesion recognition sequence
US-09-187-859-3341

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KDT 10
|||
Db 7 KDT 9

RESULT 72

US-09-187-859-3383
; Sequence 3383, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS

```
; FILE REFERENCE: 100086.407C1
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3383
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Representative cyclic modulating agent based on
;   OTHER INFORMATION: Desmocollin cell adhesion recognition sequence
US-09-187-859-3383
```

```
Query Match          27.3%;  Score 3;  DB 4;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 2.3e+03;
Matches      3;  Conservative    0;  Mismatches    0;  Indels      0;  Gaps      0;
```

```
Qy      8 KDT 10
        |||
Db      7 KDT 9
```

RESULT 73

```
US-09-187-859-3425
; Sequence 3425, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C1
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3425
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Representative cyclic modulating agent based on
;   OTHER INFORMATION: Desmocollin cell adhesion recognition sequence
US-09-187-859-3425
```

```
Query Match          27.3%;  Score 3;  DB 4;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 2.3e+03;
Matches      3;  Conservative    0;  Mismatches    0;  Indels      0;  Gaps      0;
```

```
Qy      8 KDT 10
        |||
Db      7 KDT 9
```

RESULT 74

```
US-09-187-859-3467
```

```
; Sequence 3467, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C1
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3467
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Representative cyclic modulating agent based on
;   OTHER INFORMATION: Desmocollin cell adhesion recognition sequence
US-09-187-859-3467
```

```
Query Match          27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative    0; Mismatches    0; Indels      0; Gaps      0;
```

```
Qy          8 KDT 10
            |||
Db          7 KDT 9
```

RESULT 75

```
US-09-187-859-3509
; Sequence 3509, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C1
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3509
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Representative cyclic modulating agent based on
;   OTHER INFORMATION: Desmocollin cell adhesion recognition sequence
US-09-187-859-3509
```

```
Query Match          27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative    0; Mismatches    0; Indels      0; Gaps      0;
```

Qy 8 KDT 10
 |||
Db 7 KDT 9

Search completed: April 8, 2004, 15:52:06
Job time : 12.3077 secs

OM protein - protein search, using sw model

Run on: April 8, 2004, 15:30:07 ; Search time 8.61538 Seconds
(without alignments)
122.816 Million cell updates/sec

Title: US-09-787-443A-2
Perfect score: 11
Sequence: 1 AKKERQRKDTQ 11

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283366 seqs, 96191526 residues

Word size : 0

Total number of hits satisfying chosen parameters: 226

Minimum DB seq length: 11

Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

Database : PIR_78:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	3	27.3	11	2	PT0217	T-cell receptor be
2	3	27.3	11	2	PD0441	translation elonga
3	2	18.2	11	1	EOOCC	eledoisin - curled
4	2	18.2	11	1	EOOC	eledoisin - musky
5	2	18.2	11	2	A38841	rhodopsin homolog
6	2	18.2	11	2	PQ0682	photosystem I 17.5
7	2	18.2	11	2	B26744	megascoliakinin -
8	2	18.2	11	2	D61033	ranatachykinin D -
9	2	18.2	11	2	S42449	ant1 protein - pha
10	2	18.2	11	2	JQ0395	hypothetical prote
11	2	18.2	11	2	S66606	quinoline 2-oxidor
12	2	18.2	11	2	S58244	pyrroloquinoline q
13	2	18.2	11	2	B43669	hypothetical prote

14	2	18.2	11	2	PC2372	58K heat shock pro
15	2	18.2	11	2	S33519	probable secreted
16	2	18.2	11	2	PT0081	protein QA300023 -
17	2	18.2	11	2	G61497	seed protein ws-23
18	2	18.2	11	2	S19775	wound-induced prot
19	2	18.2	11	2	S41747	chaperonin 10 homo
20	2	18.2	11	2	A34135	DNA-binding protei
21	2	18.2	11	2	A61512	variant surface gl
22	2	18.2	11	2	A26120	6-phosphofructokin
23	2	18.2	11	2	E57789	gallbladder stone
24	2	18.2	11	2	PT0287	Ig heavy chain CRD
25	2	18.2	11	2	D56979	collagen alpha 1(I
26	2	18.2	11	2	A33571	follicle-statin - bovi
27	2	18.2	11	2	S78765	ribosomal protein
28	2	18.2	11	2	S54347	tubulin beta chain
29	2	18.2	11	2	A14454	6-phosphofructokin
30	2	18.2	11	2	A61483	pyridoxal kinase (
31	2	18.2	11	2	PN0664	dystrophin-associa
32	2	18.2	11	2	PH1583	Ig H chain V-D-J r
33	2	18.2	11	2	PN0044	protein kinase C i
34	2	18.2	11	2	PH1376	T antigen variant
35	2	18.2	11	2	S53436	beta-D-galactosida
36	2	18.2	11	2	S65377	cytochrome-c oxida
37	2	18.2	11	2	PH0903	T-cell receptor be
38	2	18.2	11	2	PH0904	T-cell receptor be
39	2	18.2	11	2	PH0922	T-cell receptor be
40	2	18.2	11	2	A48973	glucoamylase A1 (E
41	2	18.2	11	2	H84082	hypothetical prote
42	2	18.2	11	4	S19015	hypothetical prote
43	1	9.1	11	1	XAVIBH	bradykinin-potenti
44	1	9.1	11	1	XASNBA	bradykinin-potenti
45	1	9.1	11	1	ECLQ2M	tachykinin II - mi
46	1	9.1	11	1	SPHO	substance P - hors
47	1	9.1	11	1	A60654	substance P - guin
48	1	9.1	11	1	GMROL	leucosulfakinin -
49	1	9.1	11	1	LFTWWE	probable trpEG lea
50	1	9.1	11	2	S66196	alcohol dehydrogen
51	1	9.1	11	2	G42762	proteasome endopep
52	1	9.1	11	2	S68392	H+-transporting tw
53	1	9.1	11	2	A33917	dihydroorotase (EC
54	1	9.1	11	2	B49164	chromogranin-B - r
55	1	9.1	11	2	JN0023	substance P - chic
56	1	9.1	11	2	S32575	ribosomal protein
57	1	9.1	11	2	A40693	transgelin - sheep
58	1	9.1	11	2	S00616	parasporal crystal
59	1	9.1	11	2	C53652	rhlR protein - Pse
60	1	9.1	11	2	S09074	cytochrome P450-4b
61	1	9.1	11	2	A57458	gene Gax protein -
62	1	9.1	11	2	A26930	ermG leader peptid
63	1	9.1	11	2	D60409	kassinin-like pept
64	1	9.1	11	2	F60409	substance P-like p
65	1	9.1	11	2	E60409	substance P-like p
66	1	9.1	11	2	YHRT	morphogenetic neur
67	1	9.1	11	2	YHHU	morphogenetic neur
68	1	9.1	11	2	YHBO	morphogenetic neur
69	1	9.1	11	2	YHXAE	morphogenetic neur
70	1	9.1	11	2	YHJFHY	morphogenetic neur

71	1	9.1	11	2	A61365	phyllokinin - Rohd
72	1	9.1	11	2	S23308	substance P - rain
73	1	9.1	11	2	S23306	substance P - Atla
74	1	9.1	11	2	B60409	kassinin-like pept
75	1	9.1	11	2	C60409	kassinin-like pept
76	1	9.1	11	2	S07203	uperolein - frog (
77	1	9.1	11	2	S07207	Crinia-angiotensin
78	1	9.1	11	2	S07201	physalaemin - frog
79	1	9.1	11	2	A61033	ranatachykinin A -
80	1	9.1	11	2	B58501	24K kidney and bla
81	1	9.1	11	2	D58502	27K bile and gallb
82	1	9.1	11	2	A58502	38K kidney stone p
83	1	9.1	11	2	C58501	42K bile stone pro
84	1	9.1	11	2	F58501	43.5K bile stone p
85	1	9.1	11	2	PQ0231	beta-glucosidase (
86	1	9.1	11	2	S04875	nifS protein - Bra
87	1	9.1	11	2	I41138	acetyl ornithine d
88	1	9.1	11	2	S42587	celF protein - Esc
89	1	9.1	11	2	S35490	type II site-speci
90	1	9.1	11	2	S21127	precorrin methyltr
91	1	9.1	11	2	S70720	trigger factor hom
92	1	9.1	11	2	S33782	acetolactate synth
93	1	9.1	11	2	B39853	LuxC protein - Pho
94	1	9.1	11	2	A58838	hemolysin - Porphy
95	1	9.1	11	2	E60691	phycobilisome 8K 1
96	1	9.1	11	2	D60691	phycobilisome 9K 1
97	1	9.1	11	2	PC2330	cycloinulooligosac
98	1	9.1	11	2	B41835	translation elonga
99	1	9.1	11	2	S14087	parasporal crystal
100	1	9.1	11	2	A44755	20alpha-hydroxyste

ALIGNMENTS

RESULT 1

PT0217

T-cell receptor beta chain V-J region (4-1-E.2) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 30-May-1997

C;Accession: PT0217

R;Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.

J. Exp. Med. 173, 1091-1097, 1991

A;Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restricted in non-obese diabetic mice.

A;Reference number: PT0209; MUID:91217621; PMID:1902501

A;Accession: PT0217

A;Molecule type: mRNA

A;Residues: 1-11 <NAK>

C;Keywords: T-cell receptor

Query Match 27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.9e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 DTQ 11

|||

Db

9 DTQ 11

RESULT 2

PD0441

translation elongation factor TU-like protein P43, mitochondrial -- mouse
(fragment)

C;Species: Mus musculus (house mouse)

C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 21-Aug-1998

C;Accession: PD0441

R;Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Morimasa, T.; Tsugita, A.
submitted to JIPID, August 1998

A;Description: Proteome analysis of mouse brain.

A;Reference number: PD0441

A;Accession: PD0441

A;Molecule type: protein

A;Residues: 1-11 <KAW>

A;Experimental source: striatum

C;Keywords: mitochondrion

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3

|||

Db 4 AKK 6

RESULT 3

EOOCC

eledoisin - curled octopus

C;Species: Eledone cirrosa, Ozaena cirrosa (curled octopus)

C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 20-Mar-1998

C;Accession: B01561; A01561

R;Anastasi, A.; Erspamer, V.

Arch. Biochem. Biophys. 101, 56-65, 1963

A;Title: The isolation and amino acid sequence of eledoisin, the active
endecapeptide of the posterior salivary glands of Eledone.

A;Reference number: A01561

A;Accession: B01561

A;Molecule type: protein

A;Residues: 1-11 <ANA>

C;Superfamily: substance P precursor

C;Keywords: amidated carboxyl end; hormone; pyroglutamic acid; salivary gland;
secretagogue; vasodilator; venom

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KD 9

||

Db 4 KD 5

RESULT 4

EOOC

eledoisin - musky octopus

C;Species: Eledone moschata, Ozaena moschata (musky octopus)

C;Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 20-Mar-1998

C;Accession: A01561

R;Anastasi, A.; Erspamer, V.

Arch. Biochem. Biophys. 101, 56-65, 1963

A;Title: The isolation and amino acid sequence of eledoisin, the active endecapeptide of the posterior salivary glands of Eledone.

A;Reference number: A01561

A;Accession: A01561

A;Molecule type: protein

A;Residues: 1-11 <ANA>

C;Superfamily: substance P precursor

C;Keywords: amidated carboxyl end; hormone; pyroglutamic acid; salivary gland; secretagogue; vasodilator; venom

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KD 9

||

Db 4 KD 5

RESULT 5

A38841

rhodopsin homolog - squid (Watasenia scintillans) (fragment)

N;Alternate names: visual pigment protein

C;Species: Watasenia scintillans (sparkling enope)

C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 31-Oct-1997

C;Accession: A38841

R;Seidou, M.; Kubota, I.; Hiraki, K.; Kito, Y.

Biochim. Biophys. Acta 957, 318-321, 1988

A;Title: Amino acid sequence of the retinal binding site of squid visual pigment.

A;Reference number: PT0063; MUID:89051045; PMID:3191148

A;Accession: A38841

A;Molecule type: protein

A;Residues: 1-11 <SEI>

C;Superfamily: vertebrate rhodopsin

C;Keywords: chromoprotein; retinal

F;3/Binding site: retinal (Lys) (covalent) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2

||

Db 2 AK 3

RESULT 6

PQ0682

photosystem I 17.5K D2 chain - common tobacco (fragment)

C;Species: *Nicotiana tabacum* (common tobacco)

C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 17-Mar-1999

C;Accession: PQ0682

R;Obokata, J.; Mikami, K.; Hayashida, N.; Nakamura, M.; Sugiura, M.

Plant Physiol. 102, 1259-1267, 1993

A;Title: Molecular heterogeneity of photosystem I. psaD, psaE, psaF, psaH and psaL are all present in isoforms in *Nicotiana* spp.

A;Reference number: PQ0667; MUID:94105345; PMID:8278548

A;Accession: PQ0682

A;Molecule type: protein

A;Residues: 1-11 <OBO>

C;Superfamily: photosystem I chain II

C;Keywords: chloroplast; photosynthesis; photosystem I; thylakoid

Query Match 18.2%; Score 2; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 3.2e+04;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KE 4

||

Db 7 KE 8

RESULT 7

B26744

megascoliakinin - garden dagger wasp

N;Alternate names: 6-Thr-bradykinin-Lys-Ala

C;Species: *Megascolia flavifrons* (garden dagger wasp)

C;Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 18-Aug-2000

C;Accession: B26744; A28609

R;Yasuhara, T.; Mantel, P.; Nakajima, T.; Piek, T.

Toxicon 25, 527-535, 1987

A;Title: Two kinins isolated from an extract of the venom reservoirs of the solitary wasp *Megascolia flavifrons*.

A;Reference number: A94322; MUID:87293024; PMID:3617088

A;Accession: B26744

A;Molecule type: protein

A;Residues: 1-11 <YAS>

R;Nakajima, T.; Piek, T.; Yashuara, T.; Mantel, P.

Toxicon 26, 34, 1988

A;Title: Two kinins isolated from the venom of *Megascolia flavifrons*.

A;Reference number: A28609

A;Accession: A28609

A;Molecule type: protein

A;Residues: 1-11 <NAK>

C;Superfamily: unassigned animal peptides

C;Keywords: bradykinin; presynaptic neurotoxin; venom

Query Match 18.2%; Score 2; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 3.2e+04;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RK 8

Db ||
 9 RK 10

RESULT 8

D61033

ranatachykinin D - bullfrog

C;Species: Rana catesbeiana (bullfrog)

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 18-Aug-2000

C;Accession: D61033; JE0429

R;Kangawa, K.; Kozawa, H.; Hino, J.; Minamino, N.; Matsuo, H.

Regul. Pept. 42(Suppl.1), S12, 1992

A;Title: Isolation of four novel tachykinins from frog (Rana catesbeiana) brain and intestine.

A;Reference number: A61033

A;Accession: D61033

A;Molecule type: protein

A;Residues: 1-11 <KAN>

R;Kozawa, H.; Hino, J.; Minamino, N.; Kangawa, K.; Matsuo, H.

Biochem. Biophys. Res. Commun. 177, 588-595, 1991

A;Title: Isolation of four novel tachykinins from frog (Rana catesbeiana) brain and intestine.

A;Reference number: JE0426; MUID:91254337; PMID:2043143

A;Accession: JE0429

A;Molecule type: protein

A;Residues: 1-11 <KOZ>

C;Superfamily: unassigned animal peptides

C;Keywords: amidated carboxyl end; neuropeptide

F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ER 5
 ||
Db 5 ER 6

RESULT 9

S42449

ant1 protein - phage P7

C;Species: phage P7

C;Date: 07-Sep-1994 #sequence_revision 26-May-1995 #text_change 08-Oct-1999

C;Accession: S42449

R;Citron, M.; Schuster, H.

Cell 62, 591-598, 1990

A;Title: The c4 repressors of bacteriophages P1 and P7 are antisense RNAs.

A;Reference number: S42448; MUID:90335968; PMID:1696181

A;Accession: S42449

A;Status: preliminary; translation not shown

A;Molecule type: DNA

A;Residues: 1-11 <CIT>

A;Cross-references: EMBL:M35139; NID:g215705; PIDN:AAA32437.1; PID:g215707

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KK 3
||
Db 2 KK 3

RESULT 10

JQ0395

hypothetical protein (nodB 3' region) - Azorhizobium caulinodans

N;Alternate names: hypothetical 1.4K protein

C;Species: Azorhizobium caulinodans

A;Note: host Sesbania rostrata

C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 03-Feb-1994

C;Accession: JQ0395

R;Goethals, K.; Gao, M.; Tomekpe, K.; Van Montagu, M.; Holsters, M.

Mol. Gen. Genet. 219, 289-298, 1989

A;Title: Common nodABC genes in Nod locus 1 of Azorhizobium caulinodans:
nucleotide sequence and plant-inducible expression.

A;Reference number: JQ0393; MUID:90136519; PMID:2615763

A;Accession: JQ0395

A;Molecule type: DNA

A;Residues: 1-11 <GOE>

A;Cross-references: GB:L18897

A;Experimental source: strain ORS571

Query Match 18.2%; Score 2; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 3.2e+04;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KK 3
||
Db 6 KK 7

RESULT 11

S66606

quinoline 2-oxidoreductase alpha chain - Comamonas testosteroni (fragment)

C;Species: Comamonas testosteroni

C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999

C;Accession: S66606

R;Schach, S.; Tshisuaka, B.; Fetzner, S.; Lingens, F.

Eur. J. Biochem. 232, 536-544, 1995

A;Title: Quinoline 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline 5,6-
dioxygenase from Comamonas testosteroni 63. The first two enzymes in quinoline
and 3-methylquinoline degradation.

A;Reference number: S66606; MUID:96035889; PMID:7556204

A;Accession: S66606

A;Molecule type: protein

A;Residues: 1-11 <SCH>

A;Experimental source: strain 63

Query Match 18.2%; Score 2; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 3.2e+04;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2

Db ||
 1 AK 2

RESULT 12

S58244

pyrroloquinoline quinone synthesis C - *Pseudomonas fluorescens* (fragment)

C;Species: *Pseudomonas fluorescens*

C;Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 08-Oct-1999

C;Accession: S58244

R;Schnider, U.; Keel, C.; Defago, G.; Haas, D.
submitted to the EMBL Data Library, May 1995

A;Description: Tn5-directed cloning of pqq genes from *Pseudomonas fluorescens*
CHA0: their involvement in the production of the antibiotic pyoluteorin.

A;Reference number: S58239

A;Accession: S58244

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-11 <SCH>

A;Cross-references: EMBL:X87299; NID:g929799; PIDN:CAA60734.1; PID:g929806

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 DT 10

||

Db 3 DT 4

RESULT 13

B43669

hypothetical protein (rhdA 5' region) - *Synechococcus* sp. (fragment)

C;Species: *Synechococcus* sp.

C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 30-Sep-1993

C;Accession: B43669

R;Laudenbach, D.E.; Ehrhardt, D.; Green, L.; Grossman, A.
J. Bacteriol. 173, 2751-2760, 1991

A;Title: Isolation and characterization of a sulfur-regulated gene encoding a
periplasmically localized protein with sequence similarity to rhodanese.

A;Reference number: A43669; MUID:91210163; PMID:1708376

A;Accession: B43669

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-11 <LAU>

A;Cross-references: GB:M65244

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2

||

Db 6 AK 7

RESULT 14

PC2372

58K heat shock protein groEL [similarity] - *Bacillus cereus* (strain ts-4)
(fragment)

C;Species: *Bacillus cereus*

C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000

C;Accession: PC2372

R;Matsuno, K.; Miyamoto, T.; Yamaguchi, K.; Sayed, M.A.; Kajiwara, T.; Hatano, S.

Biosci. Biotechnol. Biochem. 59, 231-235, 1995

A;Title: Identification of DNA-binding proteins changed after induction of sporulation in *Bacillus cereus*.

A;Reference number: PC2369; MUID:95218265; PMID:7766022

A;Accession: PC2372

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <MAS>

C;Keywords: heat shock; molecular chaperone; stress-induced protein

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2

||

Db 1 AK 2

RESULT 15

S33519

probable secreted protein - *Acholeplasma laidlawii* (fragment)

C;Species: *Acholeplasma laidlawii*

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 22-Oct-1999

C;Accession: S33519

R;Boyer, M.J.; Jarhede, T.K.; Tegman, V.; Wieslander, A.

submitted to the EMBL Data Library, June 1993

A;Description: Sequence regions from *Acholeplasma laidlawii* which restore export of beta-lactamase in *Escherichia coli*.

A;Reference number: S33518

A;Accession: S33519

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-11 <BOY>

A;Cross-references: EMBL:Z22875; NID:g311706; PIDN:CAA80495.1; PID:g311708

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KK 3

||

Db 2 KK 3

RESULT 16

PT0081

protein QA300023 - *Arabidopsis thaliana* (fragment)

C;Species: *Arabidopsis thaliana* (mouse-ear cress)

C;Date: 07-Feb-1996 #sequence_revision 19-Apr-1996 #text_change 24-Nov-1999
C;Accession: PT0081
R;Tsugita, A.; Kamo, M.; Kawakami, M.; Ohki, Y.
submitted to JIPID, December 1995
A;Description: Two dimensional electrophoresis of plant proteins and
standardization of the gel patterns.
A;Reference number: PN0173
A;Accession: PT0081
A;Molecule type: protein
A;Residues: 1-11 <TSU>
A;Experimental source: Leaf
C;Keywords: acetylated amino end
F;1/Modified site: acetylated amino end (Ser) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KE 4
||
Db 2 KE 3

RESULT 17

G61497

seed protein ws-23 - winged bean (fragment)

C;Species: Psophocarpus tetragonolobus (winged bean)

C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-Oct-1994

C;Accession: G61497

R;Hirano, H.

J. Protein Chem. 8, 115-130, 1989

A;Title: Microsequence analysis of winged bean seed proteins electroblotted from
two-dimensional gel.

A;Reference number: A61491; MUID:89351606; PMID:2765119

A;Accession: G61497

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <HIR>

C;Keywords: glycoprotein; seed

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2
||
Db 1 AK 2

RESULT 18

S19775

wound-induced protein - tomato (fragment)

C;Species: Lycopersicon esculentum (tomato)

C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Sep-1997

C;Accession: S19775

R;Parsons, B.L.

submitted to the EMBL Data Library, May 1991

A;Reference number: S19773
A;Accession: S19775
A;Molecule type: mRNA
A;Residues: 1-11 <PAR>
A;Cross-references: EMBL:X59884; NID:g19323; PID:g19324

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KK 3
||
Db 5 KK 6

RESULT 19

S41747
chaperonin 10 homolog - potato (fragment)
C;Species: Solanum tuberosum (potato)
C;Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 07-May-1999
C;Accession: S41747
R;Burt, W.J.E.; Leaver, C.J.
FEBS Lett. 339, 139-141, 1994
A;Title: Identification of a chaperonin-10 homologue in plant mitochondria.
A;Reference number: S41747; MUID:94148071; PMID:7906228
A;Accession: S41747
A;Molecule type: protein
A;Residues: 1-11 <BUR>
A;Experimental source: mitochondrion
C;Keywords: mitochondrion; molecular chaperone

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 TQ 11
||
Db 9 TQ 10

RESULT 20

A34135
DNA-binding protein p - Crithidia fasciculata mitochondrion (fragment)
C;Species: mitochondrion Crithidia fasciculata
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 07-Dec-1999
C;Accession: A34135
R;Tittawella, I.
FEBS Lett. 260, 57-61, 1990
A;Title: Kinetoplast DNA-aggregating proteins from the parasitic protozoan Crithidia fasciculata.
A;Reference number: A34135
A;Accession: A34135
A;Molecule type: protein
A;Residues: 1-11 <TIT>
C;Genetics:
A;Genome: mitochondrion
A;Genetic code: SGC6

C;Keywords: mitochondrion

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RK 8

||

Db 8 RK 9

RESULT 21

A61512

variant surface glycoprotein MITat 1.7 - Trypanosoma brucei (fragment)

C;Species: Trypanosoma brucei

C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 07-May-1999

C;Accession: A61512

R;Holder, A.A.; Cross, G.A.M.

Mol. Biochem. Parasitol. 2, 135-150, 1981

A;Title: Glycopeptides from variant surface glycoproteins of Trypanosoma brucei.
C-terminal location of antigenically cross-reacting carbohydrate moieties.

A;Reference number: A61512; MUID:81172836; PMID:6163983

A;Accession: A61512

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <HOL>

C;Keywords: glycoprotein

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 TQ 11

||

Db 5 TQ 6

RESULT 22

A26120

6-phosphofructokinase (EC 2.7.1.11) - pig roundworm (fragment)

N;Alternate names: phosphofructokinase; phosphohexokinase

C;Species: Ascaris suum (pig roundworm)

C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 28-Apr-1993

C;Accession: A26120

R;Kulkarni, G.; Rao, G.S.J.; Srinivasan, N.G.; Hofer, H.W.; Yuan, P.M.; Harris, B.G.

J. Biol. Chem. 262, 32-34, 1987

A;Title: Ascaris suum phosphofructokinase. Phosphorylation by protein kinase and
sequence of the phosphopeptide.

A;Reference number: A26120; MUID:87083467; PMID:3025208

A;Accession: A26120

A;Molecule type: protein

A;Residues: 1-11 <KUL>

C;Keywords: glycolysis; phosphotransferase

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2
||
Db 1 AK 2

RESULT 23

E57789

gallbladder stone matrix protein, 25K - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 23-Feb-1996

C;Accession: E57789

R;Binette, J.P.; Binette, M.B.

submitted to the Protein Sequence Database, February 1996

A;Description: The proteins of gallbladder stones.

A;Reference number: A57789

A;Accession: E57789

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <BIN>

Query Match 18.2%; Score 2; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 3.2e+04;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RK 8
||
Db 2 RK 3

RESULT 24

PT0287

Ig heavy chain CRD3 region (clone 4-103) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C;Accession: PT0287

R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991

A;Title: Preferential utilization of specific immunoglobulin heavy chain
diversity and joining segments in adult human peripheral blood B lymphocytes.

A;Reference number: PT0222; MUID:91108337; PMID:1899102

A;Accession: PT0287

A;Molecule type: DNA

A;Residues: 1-11 <YAM>

A;Experimental source: B lymphocyte

C;Keywords: heterotetramer; immunoglobulin

Query Match 18.2%; Score 2; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 3.2e+04;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 TQ 11
||
Db 7 TQ 8

RESULT 25

D56979

collagen alpha 1(II) chain - bovine (fragment)

N;Alternate names: collagen alpha 3(XI) chain

C;Species: Bos primigenius taurus (cattle)

C;Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 11-Jul-1997

C;Accession: D56979

R;Wu, J.J.; Eyre, D.R.

J. Biol. Chem. 270, 18865-18870, 1995

A;Title: Structural analysis of cross-linking domains in cartilage type XI collagen. Insights on polymeric assembly.

A;Reference number: A56978; MUID:95370194; PMID:7642541

A;Accession: D56979

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <WUA>

C;Keywords: pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form 3(XI))

#status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQ 6

||

Db 4 RQ 5

RESULT 26

A33571

follicle-stimulating hormone - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)

C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 30-Sep-1993

C;Accession: A33571

R;Gospodarowicz, D.; Lau, K.

Biochem. Biophys. Res. Commun. 165, 292-298, 1989

A;Title: Pituitary follicular cells secrete both vascular endothelial growth factor and follicle-stimulating hormone.

A;Reference number: A33571; MUID:90073725; PMID:2590228

A;Accession: A33571

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <GOS>

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2

||

Db 8 AK 9

RESULT 27

S78765

ribosomal protein MRP-S24, mitochondrial - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: S78765
R;Graack, H.R.
submitted to the Protein Sequence Database, July 1999
A;Reference number: S78760
A;Accession: S78765
A;Molecule type: protein
A;Residues: 1-11 <GRA>
C;Keywords: mitochondrion
F;1-11/Product: ribosomal protein MRP-S24 (fragment) #status experimental <MAT>

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KD 9
||
Db 7 KD 8

RESULT 28

S54347

tubulin beta chain - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)

C;Date: 27-Oct-1995 #sequence_revision 30-Jan-1998 #text_change 07-May-1999

C;Accession: S54347

R;Okazaki, K.; Obata, N.H.; Inoue, S.; Hidaka, H.

Biochem. J. 306, 551-555, 1995

A;Title: S100-beta is a target protein of neurocalcin delta, an abundant isoform in glial cells.

A;Reference number: S54343; MUID:95194333; PMID:7887910

A;Accession: S54347

A;Molecule type: protein

A;Residues: 1-11 <OKA>

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KD 9
||
Db 1 KD 2

RESULT 29

A14454

6-phosphofructokinase (EC 2.7.1.11) - sheep (fragment)

C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 28-Apr-1993

C;Accession: A14454

R;Fordyce, A.M.; Midwinter, G.G.; Moore, C.H.

Biochem. Soc. Trans. 7, 721-723, 1979

A;Title: The N-terminal amino acid sequence of sheep heart phosphofructokinase.

A;Reference number: A14454; MUID:80004524; PMID:157899

A;Accession: A14454

A;Molecule type: protein

A;Residues: 1-11 <FOR>
C;Keywords: glycolysis; phosphotransferase

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2
||
Db 8 AK 9

RESULT 30

A61483

pyridoxal kinase (EC 2.7.1.35) - sheep (fragment)

C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-Oct-1994

C;Accession: A61483

R;Churchich, J.E.

J. Protein Chem. 9, 613-621, 1990

A;Title: Cleavage of pyridoxal kinase into two structural domains: kinetics of proteolysis monitored by emission anisotropy.

A;Reference number: A61483; MUID:91197387; PMID:2085386

A;Accession: A61483

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <CHU>

C;Keywords: homodimer; phosphotransferase

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QR 7
||
Db 10 QR 11

RESULT 31

PN0664

dystrophin-associated glycoprotein A3a-III - rabbit (fragment)

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 07-May-1999

C;Accession: PN0664

R;Yoshida, M.; Mizuno, Y.; Nonaka, I.; Ozawa, E.

J. Biochem. 114, 634-639, 1993

A;Title: A dystrophin-associated glycoprotein, A3a (one of 43DAG doublets), is retained in Duchenne muscular dystrophy muscle.

A;Reference number: PN0662; MUID:94156881; PMID:8113213

A;Accession: PN0664

A;Molecule type: protein

A;Residues: 1-11 <YOS>

C;Comment: This protein is retained in Duchenne type muscular dystrophy muscle.

C;Keywords: glycoprotein; skeletal muscle

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 DT 10
||
Db 7 DT 8

RESULT 32

PH1583

Ig H chain V-D-J region (wild-type clone 6) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999

C;Accession: PH1583

R;Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993

A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice using a novel quantitative limiting dilution polymerase chain reaction method.

A;Reference number: PH1580; MUID:93301609; PMID:8315387

A;Accession: PH1583

A;Molecule type: DNA

A;Residues: 1-11 <LEV>

A;Experimental source: bone marrow pre-B lymphocyte

C;Keywords: immunoglobulin

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQ 6
||
Db 3 RQ 4

RESULT 33

PN0044

protein kinase C inhibitor I - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 29-Oct-1997 #sequence_revision 29-Oct-1997 #text_change 23-Jan-1998

C;Accession: PN0044

R;Kato, H.

Kawasaki Igakkaishi 22, 245-259, 1996

A;Title: Analysis of proteins isolated by two dimensional electrophoresis of mouse neuroblastoma cells.

A;Reference number: PN0041

A;Accession: PN0044

A;Molecule type: protein

A;Residues: 1-11 <KAT>

A;Experimental source: neuroblastoma cell

C;Comment: The molecular mass is 13,900 and the pI is 6.36. The amino-terminus is blocked.

C;Keywords: brain

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 DT 10
||
Db 10 DT 11

RESULT 34

PH1376

T antigen variant K-3 - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 11-May-2000

C;Accession: PH1376

R;Lill, N.L.; Judith Tevethia, M.; Hendrickson, W.G.; Tevethia, S.S.

J. Exp. Med. 176, 449-457, 1992

A;Title: Cytotoxic T lymphocytes (CTL) against a transforming gene product select for transformed cells with point mutations within sequences encoding CTL recognition epitopes.

A;Reference number: PH1373; MUID:92364547; PMID:1380062

A;Accession: PH1376

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-11 <LIL>

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KE 4
||
Db 6 KE 7

RESULT 35

S53436

beta-D-galactosidase - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 01-Aug-1995 #sequence_revision 15-May-1998 #text_change 07-May-1999

C;Accession: S53436; S53437

R;Tulsiani, D.R.P.; Skudlarek, M.D.; Araki, Y.; Orgebin-Crist, M.C.

Biochem. J. 305, 41-50, 1995

A;Title: Purification and characterization of two forms of beta-D-galactosidase from rat epididymal luminal fluid: evidence for their role in the modification of sperm plasma membrane glycoprotein(s).

A;Reference number: S53436; MUID:95126928; PMID:7826352

A;Accession: S53436

A;Molecule type: protein

A;Residues: 1-11 <TUL>

A;Experimental source: epididymal fluid

A;Note: 84K form

A;Accession: S53437

A;Molecule type: protein

A;Residues: 1-11 <TUW>

A;Experimental source: epididymal fluid

A;Note: 97K form

C;Keywords: glycoprotein

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QR 7
||
Db 6 QR 7

RESULT 36

S65377

cytochrome-c oxidase (EC 1.9.3.1) chain VIa-H, cardiac - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 16-Jul-1999

C;Accession: S65377

R;Schaegger, H.; Noack, H.; Halangk, W.; Brandt, U.; von Jagow, G.

Eur. J. Biochem. 230, 235-241, 1995

A;Title: Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-terminal sequences suggest identity of the fetal heart and the adult liver isoform.

A;Reference number: S65372; MUID:95324529; PMID:7601105

A;Accession: S65377

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <SCH>

C;Keywords: cardiac muscle; heart; oxidoreductase

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2
||
Db 3 AK 4

RESULT 37

PH0903

T-cell receptor beta chain V-D-J region (hybridoma S1C2A6) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997

C;Accession: PH0903

R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.

J. Exp. Med. 174, 1467-1476, 1991

A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic encephalomyelitis: conserved complementarity determining region 3.

A;Reference number: PH0891; MUID:92078857; PMID:1836012

A;Accession: PH0903

A;Molecule type: mRNA

A;Residues: 1-11 <GOL>

A;Experimental source: myelin basic protein-immunized T-cell

C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ER 5
||

Db 9 ER 10

RESULT 38

PH0904

T-cell receptor beta chain V-D-J region (hybridoma S22C2) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997

C;Accession: PH0904

R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.

J. Exp. Med. 174, 1467-1476, 1991

A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic encephalomyelitis: conserved complementarity determining region 3.

A;Reference number: PH0891; MUID:92078857; PMID:1836012

A;Accession: PH0904

A;Molecule type: mRNA

A;Residues: 1-11 <GOL>

A;Experimental source: myelin basic protein-immunized T-cell

C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 TQ 11

||

Db 10 TQ 11

RESULT 39

PH0922

T-cell receptor beta chain V-D-J region (isolate 8) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997

C;Accession: PH0922

R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.

J. Exp. Med. 174, 1467-1476, 1991

A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic encephalomyelitis: conserved complementarity determining region 3.

A;Reference number: PH0891; MUID:92078857; PMID:1836012

A;Accession: PH0922

A;Molecule type: mRNA

A;Residues: 1-11 <GOL>

A;Experimental source: concanavalin A-activated lymphoblast

C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 DT 10

||

Db 9 DT 10

RESULT 40

A48973

glucoamylase A1 (EC 3.2.1.-) - *Chalara paradoxa* (fragment)
C;Species: *Chalara paradoxa*
C;Date: 19-Dec-1993 #sequence_revision 25-Apr-1997 #text_change 25-Apr-1997
C;Accession: A48973
R;Monma, M.; Kainuma, K.
Carbohydr. Res. 227, 385-388, 1992
A;Title: Heterogeneity of the glucoamylase components of the raw-starch-digesting amylase from *Chalara paradoxa*.
A;Reference number: A48973; MUID:92361881; PMID:1499035
A;Accession: A48973
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-11 <MON>
A;Note: sequence extracted from NCBI backbone (NCBIP:110946)
C;Keywords: glycosidase; hydrolase

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ER 5
||
Db 10 ER 11

RESULT 41

H84082

hypothetical protein BH3464 [imported] - *Bacillus halodurans* (strain C-125)

C;Species: *Bacillus halodurans*

C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001

C;Accession: H84082

R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hiramata, C.; Nakamura, Y.; Ogasawara, N.; Kuhara, S.; Horikoshi, K.

Nucleic Acids Res. 28, 4317-4331, 2000

A;Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and genomic sequence comparison with *Bacillus subtilis*.

A;Reference number: A83650; MUID:20512582; PMID:11058132

A;Accession: H84082

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-11 <STO>

A;Cross-references: GB:AP001518; GB:BA000004; NID:g10175792; PIDN:BAB07183.1; GSPDB:GN00137

A;Experimental source: strain C-125

C;Genetics:

A;Gene: BH3464

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KE 4
||
Db 4 KE 5

RESULT 42

S19015
 hypothetical protein 11 ruvC-yebC intergenic region - Escherichia coli
 C;Species: Escherichia coli
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C;Accession: S19015
 R;Sharples, G.J.; Lloyd, R.G.
 J. Bacteriol. 173, 7711-7715, 1991
 A;Title: Resolution of Holliday junctions in Escherichia coli: identification of the ruvC gene product as a 19-kilodalton protein.
 A;Reference number: S19013; MUID:92041688; PMID:1657895
 A;Accession: S19015
 A;Molecule type: DNA
 A;Residues: 1-11 <SHA>
 A;Cross-references: EMBL:X59551; NID:g42172; PIDN:CAA42127.1; PID:g42174
 C;Comment: This is the hypothetical translation of a sequence that was not reported as a coding sequence in the complete genome.

Query Match 18.2%; Score 2; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 3.2e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2
 ||
 Db 4 AK 5

RESULT 43

XAVIBH

bradykinin-potentiating peptide - halys viper
 N;Alternate names: BPP
 C;Species: Agkistrodon halys (halys viper)
 C;Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 05-Aug-1994
 C;Accession: JC0002
 R;Chi, C.W.; Wang, S.Z.; Xu, L.G.; Wang, M.Y.; Lo, S.S.; Huang, W.D.
 Peptides 6, 339-342, 1985
 A;Title: Structure-function studies on the bradykinin potentiating peptide from Chinese snake venom (Agkistrodon halys Pallas).
 A;Reference number: JC0002; MUID:86177022; PMID:3008123
 A;Accession: JC0002
 A;Molecule type: protein
 A;Residues: 1-11 <CHI>
 C;Comment: Because this peptide both inhibits the activity of the angiotensin-converting enzyme and enhances the action of bradykinin, it is an antihypertensive agent.
 C;Superfamily: bradykinin-potentiating peptide
 C;Keywords: angiotensin-converting enzyme inhibitor; antihypertensive; bradykinin; pyroglutamic acid; venom
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6
 |
 Db 1 Q 1

RESULT 44

XASNBA

bradykinin-potentiating peptide B - mamushi

C;Species: Agkistrodon blomhoffi (mamushi)

C;Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 08-Dec-1995

C;Accession: A01254

R;Kato, H.; Suzuki, T.

Proc. Jpn. Acad. 46, 176-181, 1970

A;Reference number: A01254

A;Accession: A01254

A;Molecule type: protein

A;Residues: 1-11 <KAT>

A;Note: the sequence of the natural peptide was confirmed by the synthesis and analysis of a peptide having the identical structure and biological properties

C;Superfamily: bradykinin-potentiating peptide

C;Keywords: angiotensin-converting enzyme inhibitor; bradykinin; pyroglutamic acid; venom

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6
|
Db 1 Q 1

RESULT 45

ECLQ2M

tachykinin II - migratory locust

C;Species: Locusta migratoria (migratory locust)

C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 08-Dec-1995

C;Accession: S08266

R;Schoofs, L.; Holman, G.M.; Hayes, T.K.; Nachman, R.J.; de Loof, A.

FEBS Lett. 261, 397-401, 1990

A;Title: Locustatachykinin I and II, two novel insect neuropeptides with homology to peptides of the vertebrate tachykinin family.

A;Reference number: S08265; MUID:90184489; PMID:2311766

A;Accession: S08266

A;Molecule type: protein

A;Residues: 1-11 <SCH>

C;Superfamily: tachykinin

C;Keywords: amidated carboxyl end; neuropeptide; tachykinin

F;11/Modified site: amidated carboxyl end (Arg) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
|
Db 1 A 1

RESULT 46

SPHO

substance P - horse

C;Species: Equus caballus (domestic horse)

C;Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 23-Aug-1996

C;Accession: A01558

R;Studer, R.O.; Trzeciak, A.; Lergier, W.

Helv. Chim. Acta 56, 860-866, 1973

A;Title: Isolierung und Aminosaeuresequenz von Substanz P aus Pferdedarm.

A;Reference number: A01558

A;Accession: A01558

A;Molecule type: protein

A;Residues: 1-11 <STU>

C;Superfamily: substance P precursor

C;Keywords: amidated carboxyl end; hormone

F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 R 5
|
Db 1 R 1

RESULT 47

A60654

substance P - guinea pig

C;Species: Cavia porcellus (guinea pig)

C;Date: 14-May-1993 #sequence_revision 27-Jun-1994 #text_change 08-Dec-1995

C;Accession: A60654

R;Murphy, R.

Neuropeptides 14, 105-110, 1989

A;Title: Primary amino acid sequence of guinea-pig substance P.

A;Reference number: A60654; MUID:90044685; PMID:2478925

A;Accession: A60654

A;Molecule type: protein

A;Residues: 1-11 <MUR>

C;Superfamily: substance P precursor

C;Keywords: amidated carboxyl end; neuropeptide; tachykinin

F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 R 5
|
Db 1 R 1

RESULT 48

GMROL

leucosulfakinin - Madeira cockroach

N;Alternate names: LSK

C;Species: Leucophaea maderae (Madeira cockroach)

C;Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 13-Sep-1996

C;Accession: A01622
R;Nachman, R.J.; Holman, G.M.; Haddon, W.F.; Ling, N.
Science 234, 71-73, 1986
A;Title: Leucosulfakinin, a sulfated insect neuropeptide with homology to
gastrin and cholecystokinin.
A;Reference number: A01622; MUID:86315858; PMID:3749893
A;Accession: A01622
A;Molecule type: protein
A;Residues: 1-11 <NAC>
C;Superfamily: gastrin
C;Keywords: amidated carboxyl end; hormone; sulfoprotein
F;6/Binding site: sulfate (Tyr) (covalent) #status experimental
F;11/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 E 4
|
Db 1 E 1

RESULT 49

LFTWWE

probable trpEG leader peptide - *Thermus aquaticus*

C;Species: *Thermus aquaticus*

C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 16-Jul-1999

C;Accession: S03315

R;Sato, S.; Nakada, Y.; Kanaya, S.; Tanaka, T.

Biochim. Biophys. Acta 950, 303-312, 1988

A;Title: Molecular cloning and nucleotide sequence of *Thermus thermophilus* HB8
trpE and trpG.

A;Reference number: S03315; MUID:89000781; PMID:2844259

A;Accession: S03315

A;Molecule type: DNA

A;Residues: 1-11 <SAT>

A;Cross-references: EMBL:X07744; NID:g48261; PIDN:CAA30565.1; PID:g48262

A;Note: the source is designated as *Thermus thermophilus* HB8

C;Genetics:

A;Gene: trpL

C;Superfamily: probable trpEG leader peptide

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
|
Db 2 A 2

RESULT 50

S66196

alcohol dehydrogenase (EC 1.1.1.1) class III high affinity form - cod (*Gadus*
sp.) (fragment)

C;Species: *Gadus* sp. (cod)

C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 12-Jun-1998
C;Accession: S66196

R;Hjelmqvist, L.; Hackett, M.; Shafqat, J.; Danielsson, O.; Iida, J.;
Hendrickson, R.C.; Michel, H.; Shabanowitz, J.; Hunt, D.F.; Joernvall, H.
FEBS Lett. 367, 237-240, 1995

A;Title: Multiplicity of N-terminal structures of medium-chain alcohol
dehydrogenases. Mass-spectrometric analysis of plant, lower vertebrate and
higher vertebrate class I, II, and III forms of the enzyme.

A;Reference number: S66191; MUID:95331382; PMID:7607314

A;Accession: S66196

A;Molecule type: protein

A;Residues: 1-11 <HJE>

C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology

C;Keywords: alcohol metabolism; NAD; oxidoreductase

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 T 10

|
Db 1 T 1

RESULT 51

G42762

proteasome endopeptidase complex (EC 3.4.25.1) subunit 13 - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)

C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 17-Feb-2003

C;Accession: G42762

R;Dick, L.R.; Moomaw, C.R.; Pramanik, B.C.; DeMartino, G.N.; Slaughter, C.A.
Biochemistry 31, 7347-7355, 1992

A;Title: Identification and localization of a cysteinyl residue critical for the
trypsin-like catalytic activity of the proteasome.

A;Reference number: A42762; MUID:92378961; PMID:1510924

A;Accession: G42762

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <DIC>

A;Note: sequence extracted from NCBI backbone (NCBIP:112176)

C;Superfamily: multicatalytic endopeptidase complex chain C9

C;Keywords: hydrolase

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 K 2

|
Db 8 K 8

RESULT 52

S68392

H+-transporting two-sector ATPase (EC 3.6.3.14) chain I - Chlamydomonas
reinhardtii chloroplast (fragment)

N;Alternate names: ATP synthase chain I

C;Species: chloroplast Chlamydomonas reinhardtii
 C;Date: 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change 03-Jun-2002
 C;Accession: S68392
 R;Fiedler, H.R.; Schmid, R.; Leu, S.; Shavit, N.; Strotmann, H.
 FEBS Lett. 377, 163-166, 1995
 A;Title: Isolation of CF(0)CF(1) from Chlamydomonas reinhardtii cw15 and the N-terminal amino acid sequences of the CF(0)CF(1) subunits.
 A;Reference number: S68388; MUID:96128220; PMID:8543042
 A;Accession: S68392
 A;Molecule type: protein
 A;Residues: 1-11 <FIE>
 A;Experimental source: strain CW15
 C;Genetics:
 A;Genome: chloroplast
 C;Superfamily: H⁺-transporting ATP synthase protein 6
 C;Keywords: ATP biosynthesis; chloroplast; hydrolase; membrane-associated complex; thylakoid

Query Match 9.1%; Score 1; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 E 4
 |
 Db 1 E 1

RESULT 53

A33917

dihydroorotase (EC 3.5.2.3) - Chinese hamster (fragment)

C;Species: Cricetulus griseus (Chinese hamster)

C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 07-Nov-1997

C;Accession: A33917

R;Simmer, J.P.; Kelly, R.E.; Scully, J.L.; Grayson, D.R.; Rinker Jr., A.G.; Bergh, S.T.; Evans, D.R.

Proc. Natl. Acad. Sci. U.S.A. 86, 4382-4386, 1989

A;Title: Mammalian aspartate transcarbamylase (ATCase): sequence of the ATCase domain and interdomain linker in the CAD multifunctional polypeptide and properties of the isolated domain.

A;Reference number: A33917; MUID:89282776; PMID:2543974

A;Accession: A33917

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-11 <SIM>

A;Cross-references: GB:M23652

C;Superfamily: rudimentary enzyme; aspartate/ornithine carbamoyltransferase homology; Bacillus dihydroorotase homology; biotin carboxylase homology; carbamoyl-phosphate synthase (ammonia) homology; carbamoyl-phosphate synthase (glutamine-hydrolyzing) large chain homology; carbamoyl-phosphate synthase (glutamine-hydrolyzing) small chain homology; trpG homology

C;Keywords: hydrolase

Query Match 9.1%; Score 1; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 E 4

1
Db 2 E 2

RESULT 54

B49164

chromogranin-B - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 31-Oct-1997

C;Accession: B49164

R;Nielsen, E.; Welinder, B.S.; Madsen, O.D.

Endocrinology 129, 3147-3156, 1991

A;Title: Chromogranin-B, a putative precursor of eight novel rat glucagonoma peptides through processing at mono-, di-, or tribasic residues.

A;Reference number: A49164; MUID:92063871; PMID:1954895

A;Accession: B49164

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <NIE>

A;Note: sequence extracted from NCBI backbone (NCBIP:66370)

C;Superfamily: chromogranin B precursor

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 E 4

|

Db 4 E 4

RESULT 55

JN0023

substance P - chicken

C;Species: Gallus gallus (chicken)

C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 11-Jul-1997

C;Accession: JN0023

R;Conlon, J.M.; Katsoulis, S.; Schmidt, W.E.; Thim, L.

Regul. Pept. 20, 171-180, 1988

A;Title: [Arg3]substance P and neurokinin A from chicken small intestine.

A;Reference number: JN0023; MUID:88204263; PMID:2452461

A;Accession: JN0023

A;Molecule type: protein

A;Residues: 1-11 <CON>

C;Superfamily: substance P precursor

C;Keywords: amidated carboxyl end; tachykinin

F;11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 R 5

|

Db 1 R 1

RESULT 56

S32575

ribosomal protein S2, plastid - squawroot plastid (fragment)

C;Species: plastid *Conopholis americana* (squawroot)

C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 13-Aug-1999

C;Accession: S32575

R;Taylor, G.W.; Wolfe, K.H.; Morden, C.W.; dePamphilis, C.W.; Palmer, J.D.

Curr. Genet. 20, 515-518, 1991

A;Title: Lack of a functional plastid tRNA(Cys) gene is associated with loss of photosynthesis in a lineage of parasitic plants.

A;Reference number: S32575; MUID:92145776; PMID:1723664

A;Accession: S32575

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-11 <TAY>

A;Cross-references: EMBL:X64567; NID:g11275; PIDN:CAA45868.1; PID:g11276

C;Genetics:

A;Gene: rps2

A;Genome: plastid

C;Superfamily: *Escherichia coli* ribosomal protein S2

C;Keywords: plastid; protein biosynthesis; ribosome

Query Match 9.1%; Score 1; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.1e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 E 4

|

Db 11 E 11

RESULT 57

A40693

transgelin - sheep (fragment)

C;Species: *Ovis orientalis aries*, *Ovis ammon aries* (domestic sheep)

C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 31-Oct-1997

C;Accession: A40693

R;Shapland, C.; Hsuan, J.J.; Totty, N.F.; Lawson, D.

J. Cell Biol. 121, 1065-1073, 1993

A;Title: Purification and properties of transgelin: a transformation and shape change sensitive actin-gelling protein.

A;Reference number: A40693; MUID:93273790; PMID:8501116

A;Accession: A40693

A;Molecule type: protein

A;Residues: 1-11 <SHA>

A;Experimental source: aorta

C;Comment: This protein gels actin and is down regulated by transformation or loss of cell adherence in culture.

C;Superfamily: smooth muscle protein SM22; calponin repeat homology; smooth muscle protein SM22 homology

C;Keywords: actin binding; cytoskeleton

Query Match 9.1%; Score 1; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.1e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 K 2

Db 1 K 1

RESULT 58

S00616

parasporal crystal protein, wax moth-specific - *Bacillus thuringiensis* (strain galleriae 11-67) (fragment)

N;Alternate names: delta-endotoxin; parasporal crystal protein positive chain

C;Species: *Bacillus thuringiensis*

C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 13-Sep-1996

C;Accession: S00616

R;Chestukhina, G.G.; Kostina, L.I.; Zalunin, I.A.; Khodova, O.M.; Stepanov, V.M. FEBS Lett. 232, 249-251, 1988

A;Title: *Bacillus thuringiensis* ssp. galleriae simultaneously produces two delta-endotoxins differing strongly in primary structure and entomocidal activity.

A;Reference number: S00615

A;Accession: S00616

A;Molecule type: protein

A;Residues: 1-11 <CHE>

C;Comment: This toxin is effective against the larvae of *Galleria melonella* (greater wax moth) but not those of *Lymantria dispar* (gypsy moth).

C;Superfamily: parasporal crystal protein

C;Keywords: delta-endotoxin

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
 |
Db 4 A 4

RESULT 59

C53652

rhlR protein - *Pseudomonas aeruginosa* (fragment)

C;Species: *Pseudomonas aeruginosa*

C;Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 21-Aug-1998

C;Accession: C53652

R;Ochsner, U.A.; Fiechter, A.; Reiser, J. J. Biol. Chem. 269, 19787-19795, 1994

A;Title: Isolation, characterization, and expression in *Escherichia coli* of the *Pseudomonas aeruginosa* rhlAB genes encoding a rhamnosyltransferase involved in rhamnolipid biosurfactant synthesis.

A;Reference number: A53652; MUID:94327521; PMID:8051059

A;Accession: C53652

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-11 <OCH>

A;Cross-references: GB:L28170

C;Superfamily: sdiA regulatory protein

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 R 5
 |
Db 2 R 2

RESULT 60

S09074

cytochrome P450-4b - rat (fragment)

N;Alternate names: cytochrome P450K-5

N;Contains: oxidoreductase (EC 1.-.-.-)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 23-Apr-1993 #sequence_revision 23-Apr-1993 #text_change 05-Mar-1999

C;Accession: S09074

R;Imaoka, S.; Terano, Y.; Funae, Y.

Arch. Biochem. Biophys. 278, 168-178, 1990

A;Title: Changes in the amount of cytochrome P450s in rat hepatic microsomes with starvation.

A;Reference number: S09072; MUID:90210577; PMID:2321956

A;Accession: S09074

A;Molecule type: protein

A;Residues: 1-11 <IMA>

C;Superfamily: unassigned cytochrome P450; cytochrome P450 homology

C;Keywords: heme; microsome; monooxygenase; oxidoreductase; transmembrane protein

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 T 10
 |
Db 5 T 5

RESULT 61

A57458

gene Gax protein - mouse (fragment)

C;Species: Mus sp. (mouse)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 15-Oct-1999

C;Accession: A57458

R;Andres, V.; Fisher, S.; Wearsch, P.; Walsh, K.

Mol. Cell. Biol. 15, 4272-4281, 1995

A;Title: Regulation of Gax homeobox gene transcription by a combination of positive factors including myocyte-specific enhancer factor 2.

A;Reference number: A57458; MUID:95349593; PMID:7623821

A;Accession: A57458

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-11 <RES>

A;Cross-references: GB:S79168; NID:g1050991

C;Genetics:

A;Gene: Gax

C;Superfamily: unassigned homeobox proteins; homeobox homology

C;Keywords: DNA binding; homeobox; nucleus; transcription regulation

Query Match 9.1%; Score 1; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 E 4
|
Db 2 E 2

RESULT 62

A26930

ermG leader peptide 1 - *Bacillus sphaericus*

C;Species: *Bacillus sphaericus*

C;Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 24-Sep-1999

C;Accession: A26930

R;Monod, M.; Mohan, S.; Dubnau, D.

J. Bacteriol. 169, 340-350, 1987

A;Title: Cloning and analysis of ermG, a new macrolide-lincosamide-streptogramin B resistance element from *Bacillus sphaericus*.

A;Reference number: A91840; MUID:87083389; PMID:3025178

A;Accession: A26930

A;Molecule type: DNA

A;Residues: 1-11 <MON>

A;Cross-references: GB:M15332; NID:gl42881; PIDN:AAA22417.1; PID:gl42882

C;Superfamily: unassigned leader peptides

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 K 2
|
Db 3 K 3

RESULT 63

D60409

kassinin-like peptide K-III - frog (*Pseudophryne guentheri*)

C;Species: *Pseudophryne guentheri*

C;Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 02-Sep-2000

C;Accession: D60409

R;Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchiorri, P.; Erspamer, V.

Peptides 11, 299-304, 1990

A;Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Australian frog *Pseudophryne guentheri*.

A;Reference number: A60409; MUID:90287814; PMID:2356157

A;Accession: D60409

A;Molecule type: protein

A;Residues: 1-11 <SIM>

C;Superfamily: unassigned animal peptides

C;Keywords: amidated carboxyl end; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6
 |
Db 1 Q 1

RESULT 64

F60409

substance P-like peptide II - frog (*Pseudophryne guentheri*)

C;Species: *Pseudophryne guentheri*

C;Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 02-Sep-2000

C;Accession: F60409

R;Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.;
Melchiorri, P.; Erspamer, V.

Peptides 11, 299-304, 1990

A;Title: Six novel tachykinin- and bombesin-related peptides from the skin of
the Australian frog *Pseudophryne guentheri*.

A;Reference number: A60409; MUID:90287814; PMID:2356157

A;Accession: F60409

A;Molecule type: protein

A;Residues: 1-11 <SIM>

C;Superfamily: unassigned animal peptides

C;Keywords: amidated carboxyl end; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6
 |
Db 1 Q 1

RESULT 65

E60409

substance P-like peptide I - frog (*Pseudophryne guentheri*)

C;Species: *Pseudophryne guentheri*

C;Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 02-Sep-2000

C;Accession: E60409

R;Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.;
Melchiorri, P.; Erspamer, V.

Peptides 11, 299-304, 1990

A;Title: Six novel tachykinin- and bombesin-related peptides from the skin of
the Australian frog *Pseudophryne guentheri*.

A;Reference number: A60409; MUID:90287814; PMID:2356157

A;Accession: E60409

A;Molecule type: protein

A;Residues: 1-11 <SIM>

C;Superfamily: unassigned animal peptides

C;Keywords: amidated carboxyl end; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6
|
Db 1 Q 1

RESULT 66

YHRT

morphogenetic neuropeptide - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000

C;Accession: A01427

R;Bodenmuller, H.; Schaller, H.C.

Nature 293, 579-580, 1981

A;Title: Conserved amino acid sequence of a neuropeptide, the head activator, from coelenterates to humans.

A;Reference number: A93266; MUID:82035850; PMID:7290191

A;Accession: A01427

A;Molecule type: protein

A;Residues: 1-11 <BOD>

R;Birrr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.

FEBS Lett. 131, 317-321, 1981

A;Title: Synthesis of a new neuropeptide, the head activator from hydra.

A;Reference number: A91296; MUID:82050803; PMID:7297679

A;Contents: annotation; synthesis

A;Note: the synthetic peptide was identical with the natural peptide in chemical structure and biological activity

C;Comment: This peptide was first isolated from nerve cells of hydra and was called head activator by the authors, because it induced head-specific growth and differentiation in this animal. It has been found in mammalian intestine and hypothalamus.

C;Superfamily: unassigned animal peptides

C;Keywords: growth factor; hormone; hypothalamus; intestine; neuropeptide; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.1e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6
|
Db 1 Q 1

RESULT 67

YHHU

morphogenetic neuropeptide - human

C;Species: Homo sapiens (man)

C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000

C;Accession: B01427; A01427

R;Bodenmuller, H.; Schaller, H.C.

Nature 293, 579-580, 1981

A;Title: Conserved amino acid sequence of a neuropeptide, the head activator, from coelenterates to humans.

A;Reference number: A93266; MUID:82035850; PMID:7290191

A;Accession: B01427
 A;Molecule type: protein
 A;Residues: 1-11 <BOD>
 R;Birrr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.
 FEBS Lett. 131, 317-321, 1981
 A;Title: Synthesis of a new neuropeptide, the head activator from hydra.
 A;Reference number: A91296; MUID:82050803; PMID:7297679
 A;Contents: annotation; synthesis
 A;Note: the synthetic peptide was identical with the natural peptide in chemical structure and biological activity
 C;Comment: This peptide was first isolated from nerve cells of hydra and was called head activator because it induced head-specific growth and differentiation in this animal. It has been found in mammalian intestine and hypothalamus.
 C;Superfamily: unassigned animal peptides
 C;Keywords: blocked amino end; growth factor; hormone; hypothalamus; intestine; neuropeptide
 F;1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6
 |
 Db 1 Q 1

RESULT 68

YHBO

morphogenetic neuropeptide - bovine

C;Species: Bos primigenius taurus (cattle)

C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000

C;Accession: C01427; A01427

R;Bodenmuller, H.; Schaller, H.C.

Nature 293, 579-580, 1981

A;Title: Conserved amino acid sequence of a neuropeptide, the head activator, from coelenterates to humans.

A;Reference number: A93266; MUID:82035850; PMID:7290191

A;Accession: C01427

A;Molecule type: protein

A;Residues: 1-11 <BOD>

R;Birrr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.

FEBS Lett. 131, 317-321, 1981

A;Title: Synthesis of a new neuropeptide, the head activator from hydra.

A;Reference number: A91296; MUID:82050803; PMID:7297679

A;Contents: annotation; synthesis

A;Note: the synthetic peptide was identical with the natural peptide in chemical structure and biological activity

C;Comment: This peptide was first isolated from nerve cells of hydra and was called head activator because it induced head-specific growth and differentiation in this animal. It has been found in mammalian intestine and hypothalamus.

C;Superfamily: unassigned animal peptides

C;Keywords: blocked amino end; growth factor; hormone; hypothalamus; intestine; neuropeptide

F;1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6
|
Db 1 Q 1

RESULT 69

YHXAE

morphogenetic neuropeptide - sea anemone (*Anthopleura elegantissima*)

N;Alternate names: head activator

C;Species: *Anthopleura elegantissima*

C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000

C;Accession: A93900; A01427

R;Schaller, H.C.; Bodenmuller, H.

Proc. Natl. Acad. Sci. U.S.A. 78, 7000-7004, 1981

A;Title: Isolation and amino acid sequence of a morphogenetic peptide from hydra.

A;Reference number: A93900

A;Accession: A93900

A;Molecule type: protein

A;Residues: 1-11 <SCH>

R;Birrr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.

FEBS Lett. 131, 317-321, 1981

A;Title: Synthesis of a new neuropeptide, the head activator from hydra.

A;Reference number: A91296; MUID:82050803; PMID:7297679

A;Contents: annotation; synthesis

A;Note: the synthetic peptide was identical with the natural peptide in chemical structure and biological activity

C;Comment: This peptide was first isolated from nerve cells of hydra and was called head activator because it induced head-specific growth and differentiation in this animal. It has also been found in mammalian intestine and hypothalamus.

C;Superfamily: unassigned animal peptides

C;Keywords: growth factor; hormone; neuropeptide; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6
|
Db 1 Q 1

RESULT 70

YHJFHY

morphogenetic neuropeptide - *Hydra attenuata*

N;Alternate names: head activator

C;Species: *Hydra attenuata*

C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000

C;Accession: B93900; A01427
 R;Schaller, H.C.; Bodenmuller, H.
 Proc. Natl. Acad. Sci. U.S.A. 78, 7000-7004, 1981
 A;Title: Isolation and amino acid sequence of a morphogenetic peptide from hydra.
 A;Reference number: A93900
 A;Accession: B93900
 A;Molecule type: protein
 A;Residues: 1-11 <SCH>
 R;Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.
 FEBS Lett. 131, 317-321, 1981
 A;Title: Synthesis of a new neuropeptide, the head activator from hydra.
 A;Reference number: A91296; MUID:82050803; PMID:7297679
 A;Contents: annotation; synthesis
 A;Note: the synthetic peptide was identical with the natural peptide in chemical structure and biological activity
 C;Comment: This peptide was first isolated from nerve cells of hydra and was called head activator because it induced head-specific growth and differentiation in this animal. It has also been found in mammalian intestine and hypothalamus.
 C;Superfamily: unassigned animal peptides
 C;Keywords: growth factor; hormone; neuropeptide; pyroglutamic acid
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6
 |
 Db 1 Q 1

RESULT 71

A61365
 phyllokinin - Rohde's leaf frog
 N;Alternate names: bradykinyl-isoleucyl-tyrosine O-sulfate
 C;Species: Phyllomedusa rohdei (Rohde's leaf frog)
 C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 18-Aug-2000
 C;Accession: A61365
 R;Anastasi, A.; Bertaccini, G.; Erspamer, V.
 Br. J. Pharmacol. 27, 479-485, 1966
 A;Title: Pharmacological data on phyllokinin (bradykinyl-isoleucyl-tyrosine O-sulphate) and bradykinyl-isoleucyl-tyrosine.
 A;Reference number: A61365; MUID:67179312; PMID:5970899
 A;Accession: A61365
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-11 <ANA>
 C;Superfamily: unassigned animal peptides
 C;Keywords: sulfoprotein
 F;11/Binding site: sulfate (Tyr) (covalent) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 R 5
 |
Db 1 R 1

RESULT 72

S23308

substance P - rainbow trout

C;Species: Oncorhynchus mykiss (rainbow trout)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 18-Aug-2000

C;Accession: S23308

R;Jensen, J.; Conlon, J.M.

Eur. J. Biochem. 206, 659-664, 1992

A;Title: Substance-P-related and neurokinin-A-related peptides from the brain of the cod and trout.

A;Reference number: S23186; MUID:92298992; PMID:1376687

A;Accession: S23308

A;Molecule type: protein

A;Residues: 1-11 <JEN>

A;Experimental source: brain

C;Function:

A;Description: may play a physiological role in the regulation of cardiovascular and gastrointestinal functions

A;Note: substance P is derived by post-translational processing of preprotachykinin A

C;Superfamily: unassigned animal peptides

C;Keywords: neuropeptide; amidated carboxyl end; tachykinin

F;11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 K 2
 |
Db 1 K 1

RESULT 73

S23306

substance P - Atlantic cod

C;Species: Gadus morhua (Atlantic cod)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 18-Aug-2000

C;Accession: S23306

R;Jensen, J.; Conlon, J.M.

Eur. J. Biochem. 206, 659-664, 1992

A;Title: Substance-P-related and neurokinin-A-related peptides from the brain of the cod and trout.

A;Reference number: S23186; MUID:92298992; PMID:1376687

A;Accession: S23306

A;Molecule type: protein

A;Residues: 1-11 <JEN>

A;Experimental source: brain

C;Function:

A;Description: may play a physiological role in the regulation of cardiovascular and gastrointestinal functions

A;Note: substance P is derived by post-translational processing of preprotachykinin A
C;Superfamily: unassigned animal peptides
C;Keywords: neuropeptide; amidated carboxyl end; tachykinin
F;11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 K 2
|
Db 1 K 1

RESULT 74

B60409

kassinin-like peptide K-I - frog (*Pseudophryne guentheri*)

C;Species: *Pseudophryne guentheri*

C;Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 18-Aug-2000

C;Accession: B60409

R;Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchiorri, P.; Erspamer, V.

Peptides 11, 299-304, 1990

A;Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Australian frog *Pseudophryne guentheri*.

A;Reference number: A60409; MUID:90287814; PMID:2356157

A;Accession: B60409

A;Molecule type: protein

A;Residues: 1-11 <SIM>

A;Note: this peptide was also found in a deamidated form

C;Superfamily: unassigned animal peptides

C;Keywords: amidated carboxyl end; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;11/Modified site: amidated carboxyl end (Met) (partial) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6
|
Db 1 Q 1

RESULT 75

C60409

kassinin-like peptide K-II - frog (*Pseudophryne guentheri*)

C;Species: *Pseudophryne guentheri*

C;Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 18-Aug-2000

C;Accession: C60409

R;Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchiorri, P.; Erspamer, V.

Peptides 11, 299-304, 1990

A;Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Australian frog *Pseudophryne guentheri*.

A;Reference number: A60409; MUID:90287814; PMID:2356157

A;Accession: C60409
A;Molecule type: protein
A;Residues: 1-11 <SIM>
A;Note: this peptide was also found in a deamidated form
C;Superfamily: unassigned animal peptides
C;Keywords: amidated carboxyl end; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;11/Modified site: amidated carboxyl end (Met) (partial) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6
|
Db 1 Q 1

Search completed: April 8, 2004, 15:49:24
Job time : 8.61538 secs

OM protein - protein search, using sw model

Run on: April 8, 2004, 15:47:33 ; Search time 30.3077 Seconds
(without alignments)
95.432 Million cell updates/sec

Title: US-09-787-443A-2
Perfect score: 11
Sequence: 1 AKKERQRKDTQ 11

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1073127 seqs, 262937947 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9223

Minimum DB seq length: 11
Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					
No.	Score	Match	Length	DB	ID	Description

1	4	36.4	11	9	US-09-879-936-10	Sequence 10, Appl
2	4	36.4	11	14	US-10-304-443-118	Sequence 118, App
3	3	27.3	11	8	US-08-344-824-44	Sequence 44, Appl
4	3	27.3	11	9	US-09-780-070-37	Sequence 37, Appl
5	3	27.3	11	9	US-09-815-108-9	Sequence 9, Appli
6	3	27.3	11	9	US-09-839-666-12	Sequence 12, Appl
7	3	27.3	11	9	US-09-886-404-13	Sequence 13, Appl
8	3	27.3	11	9	US-09-805-805-8	Sequence 8, Appli
9	3	27.3	11	9	US-09-809-567-16	Sequence 16, Appl
10	3	27.3	11	9	US-09-802-109-1	Sequence 1, Appli
11	3	27.3	11	9	US-09-802-109-2	Sequence 2, Appli
12	3	27.3	11	9	US-09-802-109-3	Sequence 3, Appli
13	3	27.3	11	9	US-09-802-109-4	Sequence 4, Appli
14	3	27.3	11	9	US-09-802-109-5	Sequence 5, Appli
15	3	27.3	11	9	US-09-802-109-6	Sequence 6, Appli
16	3	27.3	11	9	US-09-802-109-8	Sequence 8, Appli
17	3	27.3	11	9	US-09-821-821-24	Sequence 24, Appl
18	3	27.3	11	9	US-09-895-943-13	Sequence 13, Appl
19	3	27.3	11	9	US-09-873-676-23	Sequence 23, Appl
20	3	27.3	11	9	US-09-891-064A-6	Sequence 6, Appli
21	3	27.3	11	9	US-09-825-414-91	Sequence 91, Appl
22	3	27.3	11	9	US-09-941-611-3	Sequence 3, Appli
23	3	27.3	11	9	US-09-867-274-23	Sequence 23, Appl
24	3	27.3	11	9	US-09-955-866-24	Sequence 24, Appl
25	3	27.3	11	9	US-09-736-743A-2	Sequence 2, Appli
26	3	27.3	11	9	US-09-984-056-103	Sequence 103, App
27	3	27.3	11	9	US-09-928-175-25	Sequence 25, Appl
28	3	27.3	11	9	US-09-995-542-13	Sequence 13, Appl
29	3	27.3	11	9	US-09-872-832-37	Sequence 37, Appl
30	3	27.3	11	9	US-09-927-850-18	Sequence 18, Appl
31	3	27.3	11	9	US-09-833-079-2	Sequence 2, Appli
32	3	27.3	11	9	US-09-833-079-17	Sequence 17, Appl
33	3	27.3	11	9	US-09-984-183-4	Sequence 4, Appli
34	3	27.3	11	9	US-09-949-196-15	Sequence 15, Appl
35	3	27.3	11	9	US-09-948-018-22	Sequence 22, Appl
36	3	27.3	11	9	US-09-995-515-14	Sequence 14, Appl
37	3	27.3	11	9	US-09-071-838-204	Sequence 204, App
38	3	27.3	11	9	US-09-895-593-13	Sequence 13, Appl
39	3	27.3	11	9	US-09-896-738-20	Sequence 20, Appl
40	3	27.3	11	9	US-09-981-286A-2	Sequence 2, Appli
41	3	27.3	11	10	US-09-798-051-10	Sequence 10, Appl
42	3	27.3	11	10	US-09-948-193-20	Sequence 20, Appl
43	3	27.3	11	10	US-09-906-393A-9	Sequence 9, Appli
44	3	27.3	11	10	US-09-134-793-2	Sequence 2, Appli
45	3	27.3	11	10	US-09-882-291-43	Sequence 43, Appl
46	3	27.3	11	10	US-09-775-052-2	Sequence 2, Appli
47	3	27.3	11	10	US-09-775-052-16	Sequence 16, Appl
48	3	27.3	11	10	US-09-775-052-52	Sequence 52, Appl
49	3	27.3	11	10	US-09-847-946A-124	Sequence 124, App
50	3	27.3	11	10	US-09-847-946A-125	Sequence 125, App
51	3	27.3	11	10	US-09-876-904A-5	Sequence 5, Appli
52	3	27.3	11	10	US-09-876-904A-10	Sequence 10, Appl
53	3	27.3	11	10	US-09-876-904A-50	Sequence 50, Appl
54	3	27.3	11	10	US-09-876-904A-111	Sequence 111, App
55	3	27.3	11	10	US-09-876-904A-200	Sequence 200, App
56	3	27.3	11	10	US-09-876-904A-232	Sequence 232, App

57	3	27.3	11	10	US-09-876-904A-237	Sequence 237, App
58	3	27.3	11	10	US-09-876-904A-273	Sequence 273, App
59	3	27.3	11	10	US-09-876-904A-354	Sequence 354, App
60	3	27.3	11	10	US-09-876-904A-434	Sequence 434, App
61	3	27.3	11	10	US-09-876-904A-591	Sequence 591, App
62	3	27.3	11	10	US-09-876-904A-597	Sequence 597, App
63	3	27.3	11	10	US-09-820-053A-113	Sequence 113, App
64	3	27.3	11	10	US-09-820-053A-139	Sequence 139, App
65	3	27.3	11	10	US-09-845-612B-20	Sequence 20, Appl
66	3	27.3	11	10	US-09-992-665-55	Sequence 55, Appl
67	3	27.3	11	10	US-09-865-548A-35	Sequence 35, Appl
68	3	27.3	11	10	US-09-997-465B-2	Sequence 2, Appli
69	3	27.3	11	10	US-09-997-465B-18	Sequence 18, Appl
70	3	27.3	11	10	US-09-911-261A-18	Sequence 18, Appl
71	3	27.3	11	10	US-09-798-053-10	Sequence 10, Appl
72	3	27.3	11	10	US-09-854-248-20	Sequence 20, Appl
73	3	27.3	11	10	US-09-962-756-1790	Sequence 1790, Ap
74	3	27.3	11	10	US-09-962-756-2008	Sequence 2008, Ap
75	3	27.3	11	12	US-09-784-553C-50	Sequence 50, Appl
76	3	27.3	11	12	US-09-784-553C-51	Sequence 51, Appl
77	3	27.3	11	12	US-09-784-553C-52	Sequence 52, Appl
78	3	27.3	11	12	US-09-784-553C-53	Sequence 53, Appl
79	3	27.3	11	12	US-09-784-553C-54	Sequence 54, Appl
80	3	27.3	11	12	US-09-784-553C-57	Sequence 57, Appl
81	3	27.3	11	12	US-09-784-553C-60	Sequence 60, Appl
82	3	27.3	11	12	US-10-232-410-11	Sequence 11, Appl
83	3	27.3	11	12	US-10-616-788-16	Sequence 16, Appl
84	3	27.3	11	12	US-09-779-791A-1	Sequence 1, Appli
85	3	27.3	11	12	US-09-822-965-17	Sequence 17, Appl
86	3	27.3	11	12	US-09-822-965-19	Sequence 19, Appl
87	3	27.3	11	12	US-09-823-418-17	Sequence 17, Appl
88	3	27.3	11	12	US-09-823-418-19	Sequence 19, Appl
89	3	27.3	11	12	US-10-622-108-16	Sequence 16, Appl
90	3	27.3	11	13	US-10-007-363-5	Sequence 5, Appli
91	3	27.3	11	14	US-10-139-833-18	Sequence 18, Appl
92	3	27.3	11	14	US-10-083-815-22	Sequence 22, Appl
93	3	27.3	11	14	US-10-108-795-28	Sequence 28, Appl
94	3	27.3	11	14	US-10-108-795-29	Sequence 29, Appl
95	3	27.3	11	14	US-10-142-356-23	Sequence 23, Appl
96	3	27.3	11	14	US-10-156-424A-14	Sequence 14, Appl
97	3	27.3	11	14	US-10-062-710-129	Sequence 129, App
98	3	27.3	11	14	US-10-044-995-3	Sequence 3, Appli
99	3	27.3	11	14	US-10-208-374-2	Sequence 2, Appli
100	3	27.3	11	14	US-10-043-487-538	Sequence 538, App

ALIGNMENTS

RESULT 1
 US-09-879-936-10
 ; Sequence 10, Application US/09879936
 ; Patent No. US20020045564A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Van Eyk, Jennifer E.
 ; APPLICANT: Mak, Alan S.
 ; APPLICANT: Cote, Graham P.

```

; TITLE OF INVENTION: Methods of Modulating Muscle Contraction
; FILE REFERENCE: 1997-021-03US
; CURRENT APPLICATION NUMBER: US/09/879,936
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/050,478
; PRIOR FILING DATE: 1997-06-23
; PRIOR APPLICATION NUMBER: 60/089,505
; PRIOR FILING DATE: 1998-06-16
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Unknown
;   FEATURE:
;   NAME/KEY: PEPTIDE
;   LOCATION: (1)..(11)
;   OTHER INFORMATION: Residues 423 to 433 of chicken gizzard caldesmon
;   NAME/KEY: PEPTIDE
;   LOCATION: (11)
;   OTHER INFORMATION: Targeted Ser phospho-amino acid
US-09-879-936-10

```

```

Query Match          36.4%; Score 4; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches      4; Conservative    0; Mismatches    0; Indels      0; Gaps      0;

```

```

Qy      1 AKKE 4
        ||||
Db      7 AKKE 10

```

RESULT 2

```

US-10-304-443-118
; Sequence 118, Application US/10304443
; Publication No. US20030170229A1
; GENERAL INFORMATION:
; APPLICANT: Smithkline Beecham Biologicals s.a.
; APPLICANT: Peptide Therapeutics Ltd.
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45173CIP
; CURRENT APPLICATION NUMBER: US/10/304,443
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: US/09/698,906A
; PRIOR FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 118
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Human peptide sequence
US-10-304-443-118

```

```

Query Match          36.4%; Score 4; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches      4; Conservative    0; Mismatches    0; Indels      0; Gaps      0;

```

Qy 4 ERQR 7
||||
Db 2 ERQR 5

RESULT 3

US-08-344-824-44

; Sequence 44, Application US/08344824
; Publication No. US20030152580A1
; GENERAL INFORMATION:
; APPLICANT: SETTE, Alessandro
; APPLICANT: SIDNEY, John
; TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
; NUMBER OF SEQUENCES: 399
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Steuart Street Tower, 20th
; STREET: Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/344,824
; FILING DATE: 23-NOV-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/278,634
; FILING DATE: 21-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 14137-80-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-344-824-44

Query Match 27.3%; Score 3; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KER 5
|||
Db 4 KER 6

RESULT 4

US-09-780-070-37

; Sequence 37, Application US/09780070

; Patent No. US20020009752A1

; GENERAL INFORMATION:

; APPLICANT: Burke, James

; APPLICANT: Strittmater, Warren

; APPLICANT: Nagai, Yoshitaka

; TITLE OF INVENTION: COMPOUNDS THAT SELECTIVELY BIND TO EXPANDED POLYGLUTAMINE
REPEAT DOMAINS

; TITLE OF INVENTION: AND METHODS OF USE THEREOF

; FILE REFERENCE: 5405.242

; CURRENT APPLICATION NUMBER: US/09/780,070

; CURRENT FILING DATE: 2001-02-09

; PRIOR APPLICATION NUMBER: 60/189,781

; PRIOR FILING DATE: 2000-03-16

; NUMBER OF SEQ ID NOS: 40

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 37

; LENGTH: 11

; TYPE: PRT

; ORGANISM: Human immunodeficiency virus

US-09-780-070-37

Query Match 27.3%; Score 3; DB 9; Length 11;

Best Local Similarity 100.0%; Pred. No. 8.3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7

|||

Db 7 RQR 9

RESULT 5

US-09-815-108-9

; Sequence 9, Application US/09815108

; Patent No. US20020009776A1

; GENERAL INFORMATION:

; APPLICANT: Saris, Christiaan M.

; APPLICANT: Sharon, Mu X.

; APPLICANT: Xia, Min

; APPLICANT: Boone, Thomas Charles

; APPLICANT: Covey, Todd

; TITLE OF INVENTION: Fibroblast Growth Factor Receptor-Like Molecules and

; TITLE OF INVENTION: Uses Thereof

; FILE REFERENCE: 99-513-A

; CURRENT APPLICATION NUMBER: US/09/815,108

; CURRENT FILING DATE: 2001-03-22

; PRIOR APPLICATION NUMBER: 60/191,379

; PRIOR FILING DATE: 2000-03-22

; NUMBER OF SEQ ID NOS: 22

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 9

; LENGTH: 11

; TYPE: PRT

; ORGANISM: Human immunodeficiency virus type 1
US-09-815-108-9

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7
|||
Db 7 RQR 9

RESULT 6

US-09-839-666-12

; Sequence 12, Application US/09839666

; Patent No. US20020025513A1

; GENERAL INFORMATION:

; APPLICANT: SALLBERG, MATTI

; TITLE OF INVENTION: ANTIGEN/ANTIBODY SPECIFICITY

; EXCHANGER

; NUMBER OF SEQUENCES: 23

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DARBY & DARBY PC

; STREET: 805 Third Avenue

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10022

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/839,666

; FILING DATE: 19-Apr-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/737,085

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Green, Reza

; REGISTRATION NUMBER: 38,475

; REFERENCE/DOCKET NUMBER: 3846/0C569

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-527-7659

; TELEFAX: 212-753-6237

; TELEX: 236687

; INFORMATION FOR SEQ ID NO: 12:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 12:

US-09-839-666-12

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QRK 8
|||
Db 1 QRK 3

RESULT 7

US-09-886-404-13
; Sequence 13, Application US/09886404
; Patent No. US20020037524A1
; GENERAL INFORMATION:
; APPLICANT: Medlock, Eugene
; APPLICANT: Yeh, Richard
; APPLICANT: Silbiger, Scott M.
; APPLICANT: Elliot, Gary S.
; APPLICANT: Nguyen, Hung Q.
; APPLICANT: Jing, Shuqian
; TITLE OF INVENTION: IL-17 Like Molecules and Uses Thereof
; FILE REFERENCE: 01017/37128B
; CURRENT APPLICATION NUMBER: US/09/886,404
; CURRENT FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 09/810,384
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/266,159
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/213,125
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide of HIV
; OTHER INFORMATION: TAT protein
US-09-886-404-13

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7
|||
Db 7 RQR 9

RESULT 8

US-09-805-805-8
; Sequence 8, Application US/09805805
; Patent No. US20020037557A1
; GENERAL INFORMATION:
; APPLICANT: Bass, Michael B.

```
; APPLICANT: Jing, Shuqian
; TITLE OF INVENTION: Fibroblast Growth Factor-Like Molecules and Uses
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 01-006-A1
; CURRENT APPLICATION NUMBER: US/09/805,805
; CURRENT FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: 60/188,786
; PRIOR FILING DATE: 2000-03-13
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-805-805-8
```

```
Query Match          27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy      5 RQR 7
        |||
Db      7 RQR 9
```

RESULT 9

US-09-809-567-16

```
; Sequence 16, Application US/09809567
; Patent No. US20020045213A1
; GENERAL INFORMATION:
; APPLICANT: Jing, Shuqian
; TITLE OF INVENTION: IL-17 Receptor Like Molecules and Uses Thereof
; FILE REFERENCE: 01017/36916A
; CURRENT APPLICATION NUMBER: US/09/809,567
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/724,460
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/189,816
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide
US-09-809-567-16
```

```
Query Match          27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy      5 RQR 7
        |||
Db      7 RQR 9
```


RESULT 10

US-09-802-109-1

```
; Sequence 1, Application US/09802109
; Patent No. US20020058611A1
; GENERAL INFORMATION:
; APPLICANT: Stein, Stanley
; TITLE OF INVENTION: CARRIER FOR IN VIVO DELIVERY OF A THERAPEUTIC
; FILE REFERENCE: 601-1-083
; CURRENT APPLICATION NUMBER: US/09/802,109
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 09/044,411
; PRIOR FILING DATE: 1998-03-19
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; FEATURE:
; OTHER INFORMATION: Internal sequence from the Tat protein, but with
; OTHER INFORMATION: an extra Cys not found in natural protein.
; NAME/KEY: SITE
; LOCATION: (10)
; OTHER INFORMATION: Xaa is either Cys(biotin) or Lys(biotin) at this
; OTHER INFORMATION: position.
; NAME/KEY: BINDING
; LOCATION: (10)
; OTHER INFORMATION: Either Cys(biotin) or Lys(biotin) at this
; OTHER INFORMATION: position.
; OTHER INFORMATION: Peptide has an N-terminal carboxylic acid residue.
; OTHER INFORMATION: Peptide has a C-terminal amide group.
```

US-09-802-109-1

```
Query Match          27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches      3; Conservative    0; Mismatches    0; Indels      0; Gaps      0;
```

```
Qy      5 RQR 7
      |||
Db      5 RQR 7
```

RESULT 11

US-09-802-109-2

```
; Sequence 2, Application US/09802109
; Patent No. US20020058611A1
; GENERAL INFORMATION:
; APPLICANT: Stein, Stanley
; TITLE OF INVENTION: CARRIER FOR IN VIVO DELIVERY OF A THERAPEUTIC
; FILE REFERENCE: 601-1-083
; CURRENT APPLICATION NUMBER: US/09/802,109
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 09/044,411
; PRIOR FILING DATE: 1998-03-19
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
```

```

; SEQ ID NO 2
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Human immunodeficiency virus type 1
;   FEATURE:
;   OTHER INFORMATION: Internal sequence from the Tat protein, but with
;   OTHER INFORMATION: two extra Cys residues not found in thenatural
;   OTHER INFORMATION: protein.
;   NAME/KEY: BINDING
;   LOCATION: (10)
;   OTHER INFORMATION: Cys(biotin)
;   OTHER INFORMATION: Peptide has an N-terminal acetyl group.
;   OTHER INFORMATION: Peptide has a C-terminal amide group.
US-09-802-109-2

```

```

Query Match          27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches      3; Conservative    0; Mismatches    0; Indels      0; Gaps      0;

```

```

Qy          5 RQR 7
            |||
Db          5 RQR 7

```

RESULT 12

```

US-09-802-109-3
; Sequence 3, Application US/09802109
; Patent No. US20020058611A1
; GENERAL INFORMATION:
; APPLICANT: Stein, Stanley
; TITLE OF INVENTION: CARRIER FOR IN VIVO DELIVERY OF A THERAPEUTIC
; FILE REFERENCE: 601-1-083
; CURRENT APPLICATION NUMBER: US/09/802,109
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 09/044,411
; PRIOR FILING DATE: 1998-03-19
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Human immunodeficiency virus type 1
;   FEATURE:
;   OTHER INFORMATION: Internal sequence from the Tat protein, but with
;   OTHER INFORMATION: an extra Lys and an extra Cys not found in the
;   OTHER INFORMATION: natural protein.
;   NAME/KEY: BINDING
;   LOCATION: (10)
;   OTHER INFORMATION: Lys(biotin)
;   OTHER INFORMATION: Peptide has an N-terminal acetyl group.
;   OTHER INFORMATION: Peptide has a C-terminal amide group.
US-09-802-109-3

```

```

Query Match          27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches      3; Conservative    0; Mismatches    0; Indels      0; Gaps      0;

```

Qy 5 RQR 7
|||
Db 5 RQR 7

RESULT 13

US-09-802-109-4

; Sequence 4, Application US/09802109
; Patent No. US20020058611A1
; GENERAL INFORMATION:
; APPLICANT: Stein, Stanley
; TITLE OF INVENTION: CARRIER FOR IN VIVO DELIVERY OF A THERAPEUTIC
; FILE REFERENCE: 601-1-083
; CURRENT APPLICATION NUMBER: US/09/802,109
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 09/044,411
; PRIOR FILING DATE: 1998-03-19
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; FEATURE:
; OTHER INFORMATION: Internal sequence from the Tat protein, but with
; OTHER INFORMATION: two extra Cys not found in the natural protein.
; NAME/KEY: SITE
; LOCATION: (10)
; OTHER INFORMATION: Cys is the D isomer at this position.
; NAME/KEY: BINDING
; LOCATION: (10)
; OTHER INFORMATION: D-Cys(biotin)
; OTHER INFORMATION: Peptide has an N-terminal acetyl group.
; OTHER INFORMATION: Peptide has a C-terminal amide group.
US-09-802-109-4

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7
|||
Db 5 RQR 7

RESULT 14

US-09-802-109-5

; Sequence 5, Application US/09802109
; Patent No. US20020058611A1
; GENERAL INFORMATION:
; APPLICANT: Stein, Stanley
; TITLE OF INVENTION: CARRIER FOR IN VIVO DELIVERY OF A THERAPEUTIC
; FILE REFERENCE: 601-1-083
; CURRENT APPLICATION NUMBER: US/09/802,109
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 09/044,411
; PRIOR FILING DATE: 1998-03-19

```

; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; FEATURE:
; OTHER INFORMATION: Internal sequence from the Tat protein, but with
; OTHER INFORMATION: an extra Lys and an extra Cys not found in the
; OTHER INFORMATION: natural protein.
; NAME/KEY: SITE
; LOCATION: (10)
; OTHER INFORMATION: Lys is D isomer at this position.
; NAME/KEY: BINDING
; LOCATION: (10)
; OTHER INFORMATION: D-Lys(biotin)
; OTHER INFORMATION: Peptide has an N-terminal acetyl group.
; OTHER INFORMATION: Peptide has a C-terminal amide group.
US-09-802-109-5

```

```

Query Match          27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches      3; Conservative    0; Mismatches    0; Indels      0; Gaps      0;

```

```

Qy      5 RQR 7
        |||
Db      5 RQR 7

```

```

RESULT 15
US-09-802-109-6
; Sequence 6, Application US/09802109
; Patent No. US20020058611A1
; GENERAL INFORMATION:
; APPLICANT: Stein, Stanley
; TITLE OF INVENTION: CARRIER FOR IN VIVO DELIVERY OF A THERAPEUTIC
; FILE REFERENCE: 601-1-083
; CURRENT APPLICATION NUMBER: US/09/802,109
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 09/044,411
; PRIOR FILING DATE: 1998-03-19
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; FEATURE:
; OTHER INFORMATION: Same as Sequence ID 3, but with a substitution of
; OTHER INFORMATION: Arg to Gln.
; NAME/KEY: SITE
; LOCATION: (10)
; OTHER INFORMATION: Lys is the D isomer at this position.
; NAME/KEY: BINDING
; LOCATION: (10)
; OTHER INFORMATION: D-Lys(biotin)
; OTHER INFORMATION: Peptide has an N-terminal acetyl group.

```

; OTHER INFORMATION: Peptide has a C-terminal amide group.
US-09-802-109-6

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7
|||
Db 5 RQR 7

RESULT 16

US-09-802-109-8

; Sequence 8, Application US/09802109
; Patent No. US20020058611A1
; GENERAL INFORMATION:
; APPLICANT: Stein, Stanley
; TITLE OF INVENTION: CARRIER FOR IN VIVO DELIVERY OF A THERAPEUTIC
; FILE REFERENCE: 601-1-083
; CURRENT APPLICATION NUMBER: US/09/802,109
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 09/044,411
; PRIOR FILING DATE: 1998-03-19
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; FEATURE:
; OTHER INFORMATION: All amino acids in this sequence are D amino acid.
; NAME/KEY: BINDING
; LOCATION: (2)
; OTHER INFORMATION: D-Lys(biotin)
; OTHER INFORMATION: Peptide has an N-terminal acetyl group.
; OTHER INFORMATION: Peptide has a C-terminal amide group.
US-09-802-109-8

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7
|||
Db 5 RQR 7

RESULT 17

US-09-821-821-24

; Sequence 24, Application US/09821821
; Patent No. US20020064823A1
; GENERAL INFORMATION:
; APPLICANT: Welcher, Andrew A.
; APPLICANT: Calzone, Frank J.
; TITLE OF INVENTION: CD20/IgE-Receptor Like Molecules and Uses Thereof
; FILE REFERENCE: 01017/36938A

; CURRENT APPLICATION NUMBER: US/09/821,821
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: US 09/723,258
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: US 60/193,728
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide
US-09-821-821-24

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7
|||
Db 7 RQR 9

RESULT 18

US-09-895-943-13
; Sequence 13, Application US/09895943
; Patent No. US20020068323A1
; GENERAL INFORMATION:
; APPLICANT: Saris, Chris
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: Thymic Stromal Lymphopoietin Receptor Molecules and
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: 00-514-C
; CURRENT APPLICATION NUMBER: US/09/895,943
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: 60/214,866
; PRIOR FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-895-943-13

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7
|||
Db 7 RQR 9

RESULT 19

US-09-873-676-23
 ; Sequence 23, Application US/09873676
 ; Patent No. US20020077289A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MacDonald, Nicholas J.
 ; APPLICANT: Sim, Kim L.
 ; TITLE OF INVENTION: Angiostatin and Endostatin Binding Proteins and Methods
 of Use
 ; FILE REFERENCE: 05213-0378 (43170-259333)
 ; CURRENT APPLICATION NUMBER: US/09/873,676
 ; CURRENT FILING DATE: 2001-06-04
 ; PRIOR APPLICATION NUMBER: US 60/209,065
 ; PRIOR FILING DATE: 2000-06-02
 ; PRIOR APPLICATION NUMBER: US 60/289,387
 ; PRIOR FILING DATE: 2001-05-08
 ; NUMBER OF SEQ ID NOS: 123
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 23
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: synthetic binding peptide
 US-09-873-676-23

Query Match 27.3%; Score 3; DB 9; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RKD 9
 |||
 Db 5 RKD 7

RESULT 20
 US-09-891-064A-6
 ; Sequence 6, Application US/09891064A
 ; Patent No. US20020082391A1
 ; GENERAL INFORMATION:
 ; APPLICANT: James M. Anderson
 ; APPLICANT: Christina M. Van Itallie
 ; TITLE OF INVENTION: Human Occludin, Its Uses and Enhancement of Drug
 ; TITLE OF INVENTION: Absorption Using Occludin Inhibitors
 ; FILE REFERENCE: OCR-754.CIP
 ; CURRENT APPLICATION NUMBER: US/09/891,064A
 ; CURRENT FILING DATE: 2001-06-25
 ; PRIOR APPLICATION NUMBER: US 09/142,732
 ; PRIOR FILING DATE: 1998-09-15
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: MS DOS
 ; SEQ ID NO 6
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: peptide
 ; OTHER INFORMATION: construct used in experiments

US-09-891-064A-6

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RKD 9
|||
Db 7 RKD 9

RESULT 21

US-09-825-414-91

; Sequence 91, Application US/09825414
; Patent No. US20020083489A1
; GENERAL INFORMATION:
; APPLICANT: Collmer, Alan
; APPLICANT: Alfano, James R.
; APPLICANT: Charkowski, Amy O.
; TITLE OF INVENTION: DNA MOLECULES AND POLYPEPTIDES OF PSEUDOMONAS SYRINGAE
; TITLE OF INVENTION: HRP PATHOGENICITY ISLAND AND THEIR USES
; FILE REFERENCE: 19603/3243
; CURRENT APPLICATION NUMBER: US/09/825,414
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/194,160
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: 60/224,604
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/249,548
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 91
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: human
; OTHER INFORMATION: immunodeficiency virus TAT protein, transduction
; OTHER INFORMATION: domain

US-09-825-414-91

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7
|||
Db 7 RQR 9

RESULT 22

US-09-941-611-3

; Sequence 3, Application US/09941611
; Patent No. US20020106640A1
; GENERAL INFORMATION:
; APPLICANT: DELEYS, ROBERT J


```

;          POLLET, DIRK
;          MAERTENS, GEERT
;          VAN HEUVERSWUN, HUGO
;  TITLE OF INVENTION: SYNTHETIC ANTIGENS FOR THE DETECTION OF
;                      ANTIBODIES TO HEPATITIS C VIRUS
;  NUMBER OF SEQUENCES: 23
;  CORRESPONDENCE ADDRESS:
;      ADDRESSEE: NIXON & VANDERHYE P.C.
;      STREET: 1100 NORTH GLEBE ROAD
;      CITY: ARLINGTON
;      STATE: VA
;      COUNTRY: USA
;      ZIP: 22201
;  COMPUTER READABLE FORM:
;      MEDIUM TYPE: Floppy disk
;      COMPUTER: IBM PC compatible
;      OPERATING SYSTEM: PC-DOS/MS-DOS
;      SOFTWARE: PatentIn Release #1.0, Version #1.30
;  CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/09/941,611
;      FILING DATE: 30-Aug-2001
;      CLASSIFICATION: <Unknown>
;  PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 08/391,671
;      FILING DATE: 1995-02-21
;      APPLICATION NUMBER: WO PCT/EP91/02409
;      FILING DATE: 13-DEC-1991
;      APPLICATION NUMBER: EP 90124241.2
;      FILING DATE: 14-DEC-1990
;  ATTORNEY/AGENT INFORMATION:
;      NAME: SADOFF, B.J.
;      REGISTRATION NUMBER: 36,663
;      REFERENCE/DOCKET NUMBER: 1487-5
;  TELECOMMUNICATION INFORMATION:
;      TELEPHONE: 7038164000
;      TELEFAX: 7038164100
;  INFORMATION FOR SEQ ID NO: 3:
;      SEQUENCE CHARACTERISTICS:
;          LENGTH: 11 amino acids
;          TYPE: amino acid
;          STRANDEDNESS: single
;          TOPOLOGY: linear
;      MOLECULE TYPE: peptide
;      SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-941-611-3

```

```

Query Match          27.3%;  Score 3;  DB 9;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 8.3e+03;
Matches      3;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy      6 QRK 8
      |||
Db      1 QRK 3

```

```

RESULT 23
US-09-867-274-23

```

```

; Sequence 23, Application US/09867274
; Patent No. US20020106650A1
; GENERAL INFORMATION:
; APPLICANT: Paszty, Christopher
; APPLICANT: Gao, Yongming
; TITLE OF INVENTION: Cysteine Knot Polypeptides: Cloaked-2 Molecules and Uses
Thereof
; FILE REFERENCE: 01017/37428
; CURRENT APPLICATION NUMBER: US/09/867,274
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 60/208,550
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/223,542
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV TAT peptide
US-09-867-274-23

```

```

Query Match          27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      5 RQR 7
      |||
Db      7 RQR 9

```

```

RESULT 24
US-09-955-866-24
; Sequence 24, Application US/09955866
; Patent No. US20020107363A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Michael
; APPLICANT: Sullivan, John K.
; APPLICANT: Holst, Paige
; APPLICANT: Yoshinaga, Steven Kiyoshi
; TITLE OF INVENTION: B7-Like Polypeptides and Uses Thereof
; FILE REFERENCE: 00,759-A
; CURRENT APPLICATION NUMBER: US/09/955,866
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/233,867
; PRIOR FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-955-866-24

```

```

Query Match          27.3%; Score 3; DB 9; Length 11;

```

Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7
|||
Db 7 RQR 9

RESULT 25

US-09-736-743A-2

; Sequence 2, Application US/09736743A
; Patent No. US20020110869A1
; GENERAL INFORMATION:
; APPLICANT: KOVESDI, IMRE
; APPLICANT: BRUDER, JOSEPH T
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING CHIMERIC PROTEIN AND RELATED
VECTOR, CELL AND
; TITLE OF INVENTION: METHOD OF EXPRESSION
; FILE REFERENCE: 203591
; CURRENT APPLICATION NUMBER: US/09/736,743A
; CURRENT FILING DATE: 2000-12-17
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-09-736-743A-2

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7
|||
Db 5 RQR 7

RESULT 26

US-09-984-056-103

; Sequence 103, Application US/09984056
; Patent No. US20020120106A1
; GENERAL INFORMATION:
; APPLICANT: BOGOCH, SAMUEL
; APPLICANT: BOGOCH, ELENORE S.
; TITLE OF INVENTION: ANTHRAX AND SMALL POX REPLIKINS AND METHODS OF USE
; FILE REFERENCE: 09425-46903
; CURRENT APPLICATION NUMBER: US/09/984,056
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/146,755
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 09/817,144
; PRIOR FILING DATE: 2001-03-27

; PRIOR APPLICATION NUMBER: 08/198,139
; PRIOR FILING DATE: 1994-02-17
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: PatentIn 2.1
; SEQ ID NO 103
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Variola virus
US-09-984-056-103

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KER 5
|||
Db 1 KER 3

RESULT 27

US-09-928-175-25

; Sequence 25, Application US/09928175
; Patent No. US20020123618A1
; GENERAL INFORMATION:
; APPLICANT: Paszty, Christopher J.
; APPLICANT: Gong, Jianhua
; APPLICANT: Daugherty, Betsy
; APPLICANT: Rogers, No. US20020123618Alma
; TITLE OF INVENTION: Leucine-Rich G Protein Coupled Receptor-8 Molecules and
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: 00-1229
; CURRENT APPLICATION NUMBER: US/09/928,175
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/224,455
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-928-175-25

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7
|||
Db 7 RQR 9

RESULT 28

US-09-995-542-13

; Sequence 13, Application US/09995542
; Patent No. US20020127647A1
; GENERAL INFORMATION:

```
; APPLICANT: Shutter, John
; APPLICANT: Ulias, Laarni
; TITLE OF INVENTION: ATP-Binding Cassette Transporter-Like Molecules and
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: 00-658-A
; CURRENT APPLICATION NUMBER: US/09/995,542
; CURRENT FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: 60/253,520
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-995-542-13
```

```
Query Match          27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy      5 RQR 7
        |||
Db      7 RQR 9
```

RESULT 29

US-09-872-832-37

```
; Sequence 37, Application US/09872832
; Patent No. US20020131960A1
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan-Kettering Cancer Center
; TITLE OF INVENTION: ARTIFICIAL ANTIGEN PRESENTING CELLS AND METHODS OF USE
THEREOF
; FILE REFERENCE: 830002-2003.1
; CURRENT APPLICATION NUMBER: US/09/872,832
; CURRENT FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 60/209,157
; PRIOR FILING DATE: 2000-02-06
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 37
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-872-832-37
```

```
Query Match          27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy      3 KER 5
        |||
Db      4 KER 6
```

RESULT 30

US-09-927-850-18
 ; Sequence 18, Application US/09927850
 ; Patent No. US20020137137A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Welcher, Andrew
 ; APPLICANT: Wen, Duanzhi
 ; APPLICANT: Kelly, Michael
 ; TITLE OF INVENTION: Interferon-Like Molecules and Uses Thereof
 ; FILE REFERENCE: 99,372-F
 ; CURRENT APPLICATION NUMBER: US/09/927,850
 ; CURRENT FILING DATE: 2001-08-10
 ; PRIOR APPLICATION NUMBER: 09/724,860
 ; PRIOR FILING DATE: 2000-11-28
 ; PRIOR APPLICATION NUMBER: 60/169,720
 ; PRIOR FILING DATE: 1999-12-08
 ; NUMBER OF SEQ ID NOS: 39
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 18
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Human immunodeficiency virus type 1
 US-09-927-850-18

Query Match 27.3%; Score 3; DB 9; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7
 |||
 Db 7 RQR 9

RESULT 31
 US-09-833-079-2
 ; Sequence 2, Application US/09833079
 ; Patent No. US20020142008A1
 ; GENERAL INFORMATION:
 ; APPLICANT: O'HANLEY, PETER
 ; APPLICANT: DENICH, KENNETH
 ; APPLICANT: SCHMIDT, M. ALEXANDER
 ; TITLE OF INVENTION: IMMUNOGENIC PILI PRESENTING FOREIGN PEPTIDES, THEIR
 ; TITLE OF INVENTION: PRODUCTION AND USE
 ; FILE REFERENCE: 050939/0104
 ; CURRENT APPLICATION NUMBER: US/09/833,079
 ; CURRENT FILING DATE: 2001-04-12
 ; NUMBER OF SEQ ID NOS: 39
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; OTHER INFORMATION: peptide
 US-09-833-079-2

Query Match 27.3%; Score 3; DB 9; Length 11;

Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
|||
Db 8 AKK 10

RESULT 32

US-09-833-079-17

; Sequence 17, Application US/09833079
; Patent No. US20020142008A1
; GENERAL INFORMATION:
; APPLICANT: O'HANLEY, PETER
; APPLICANT: DENICH, KENNETH
; APPLICANT: SCHMIDT, M. ALEXANDER
; TITLE OF INVENTION: IMMUNOGENIC PILI PRESENTING FOREIGN PEPTIDES, THEIR
; TITLE OF INVENTION: PRODUCTION AND USE
; FILE REFERENCE: 050939/0104
; CURRENT APPLICATION NUMBER: US/09/833,079
; CURRENT FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-833-079-17

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
|||
Db 8 AKK 10

RESULT 33

US-09-984-183-4

; Sequence 4, Application US/09984183
; Patent No. US20020142983A1
; GENERAL INFORMATION:
; APPLICANT: AGRAWAL, BABITA
; APPLICANT: LONGENECKER, MICHAEL B.
; TITLE OF INVENTION: MUC-1 ANTAGONISTS AND METHODS OF TREATING IMMUNE
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: 042881/0130
; CURRENT APPLICATION NUMBER: US/09/984,183
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/457,354
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/111,973
; PRIOR FILING DATE: 1998-12-11

; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-09-984-183-4

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7
|||
Db 7 RQR 9

RESULT 34

US-09-949-196-15

; Sequence 15, Application US/09949196
; Patent No. US20020147145A1
; GENERAL INFORMATION:
; APPLICANT: Zealand Pharmaceuticals A/S
; TITLE OF INVENTION: MATERIALS AND METHODS RELATING TO THE DEGRADATION OF
Cdc25A IN RESPONSE
; TITLE OF INVENTION: TO DNA DAMAGE
; FILE REFERENCE: 55888 (45487)
; CURRENT APPLICATION NUMBER: US/09/949,196
; CURRENT FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide
sequence
US-09-949-196-15

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7
|||
Db 7 RQR 9

RESULT 35

US-09-948-018-22

; Sequence 22, Application US/09948018
; Patent No. US20020150977A1
; GENERAL INFORMATION:
; APPLICANT: Theill et al
; TITLE OF INVENTION: TNF RECEPTOR-LIKE MOLECULES AND USES THEREOF
; FILE REFERENCE: 01017/37677

; CURRENT APPLICATION NUMBER: US/09/948,018
; CURRENT FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/230,191
; PRIOR FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Peptide of HIV TAT protein
US-09-948-018-22

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7
|||
Db 7 RQR 9

RESULT 36

US-09-995-515-14

; Sequence 14, Application US/09995515
; Patent No. US20020151695A1
; GENERAL INFORMATION:
; APPLICANT: Jing, Shuqian
; TITLE OF INVENTION: Transforming Growth Factor-Beta-Related Molecules and
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: 00-659-A
; CURRENT APPLICATION NUMBER: US/09/995,515
; CURRENT FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: 60/253,476
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-995-515-14

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7
|||
Db 7 RQR 9

RESULT 37

US-09-071-838-204

; Sequence 204, Application US/09071838
; Patent No. US20020152501A1
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.

```

; APPLICANT: Ohad, Nir
; APPLICANT: Kiyosue, Tomohiro
; APPLICANT: Yadegari, Ramin
; APPLICANT: Margossian, Linda
; APPLICANT: Harada, John
; APPLICANT: Goldberg, Robert B.
; TITLE OF INVENTION: Nucleic Acids That Control Seed and
; TITLE OF INVENTION: Fruit Development in Plants
; NUMBER OF SEQUENCES: 324
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,838
; FILING DATE: 01-MAY-1998
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 023070-086100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 204:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-071-838-204

```

```

Query Match          27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      7 RKD 9
      |||
Db      3 RKD 5

```

```

RESULT 38
US-09-895-593-13
; Sequence 13, Application US/09895593
; Patent No. US20020160949A1
; GENERAL INFORMATION:
; APPLICANT: Pandey, Akhilesh
; APPLICANT: Ozaki, Katsutoshi
; APPLICANT: Baumann, Heinz

```

```

; APPLICANT: Levin, Steven D.
; APPLICANT: Farr, Andrew G.
; APPLICANT: Ziegler, Steven F.
; APPLICANT: Leonard, Warren J.
; APPLICANT: Lodish, Harvey F.
; TITLE OF INVENTION: Thymic Stromal Lymphopoietin Receptor Molecules and
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: 00-514-E
; CURRENT APPLICATION NUMBER: US/09/895,593
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: 60/215,658
; PRIOR FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-895-593-13

```

```

Query Match          27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      5 RQR 7
        |||
Db      7 RQR 9

```

RESULT 39

```

US-09-896-738-20
; Sequence 20, Application US/09896738
; Patent No. US20020165347A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Michael
; APPLICANT: Sullivan, John K.
; APPLICANT: Fang, Mei
; TITLE OF INVENTION: B7-Like Molecules and Uses Thereof
; FILE REFERENCE: 00-513-A
; CURRENT APPLICATION NUMBER: US/09/896,738
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/215,645
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-896-738-20

```

```

Query Match          27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      5 RQR 7
        |||

```

Db 7 RQR 9

RESULT 40

US-09-981-286A-2
; Sequence 2, Application US/09981286A
; Publication No. US20020192799A1
; GENERAL INFORMATION:
; APPLICANT: Watowich, Stanley J.
; APPLICANT: Weaver, Scott C.
; APPLICANT: Davey, Robert A.
; TITLE OF INVENTION: Drug Discovery Methods
; FILE REFERENCE: 265.00260101
; CURRENT APPLICATION NUMBER: US/09/981,286A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/240,187
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cell-permeant polypeptide
US-09-981-286A-2

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7
|||
Db 7 RQR 9

RESULT 41

US-09-798-051-10
; Sequence 10, Application US/09798051
; Publication No. US20030008961A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Ke
; APPLICANT: Cam, Linh
; APPLICANT: Nakayama, Naoki
; TITLE OF INVENTION: Chordin-Like-2 Molecules and Uses Thereof
; FILE REFERENCE: 01-005
; CURRENT APPLICATION NUMBER: US/09/798,051
; CURRENT FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-798-051-10

Query Match 27.3%; Score 3; DB 10; Length 11;

Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7
|||
Db 7 RQR 9

RESULT 42

US-09-948-193-20

; Sequence 20, Application US/09948193
; Publication No. US20030027335A1
; GENERAL INFORMATION:
; APPLICANT: Ruley, H. Earl
; APPLICANT: Jo, Daewoong
; TITLE OF INVENTION: Genome Engineering by Cell-Permeable DNA
; TITLE OF INVENTION: Site-Specific Recombinases
; FILE REFERENCE: 22000.0109U2
; CURRENT APPLICATION NUMBER: US/09/948,193
; CURRENT FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 60/230,690
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus
; FEATURE:
; OTHER INFORMATION: Description: MTS from HIV Tat
US-09-948-193-20

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7
|||
Db 7 RQR 9

RESULT 43

US-09-906-393A-9

; Sequence 9, Application US/09906393A
; Publication No. US20030039970A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Zhou
; APPLICANT: Xiao, Wuhan
; TITLE OF INVENTION: METHOD OF PROGNOSING CANCER AND THE PROTEINS INVOLVED
; FILE REFERENCE: 1720-1-001CIP
; CURRENT APPLICATION NUMBER: US/09/906,393A
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/218,761
; PRIOR FILING DATE: 2000-07-17
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9

; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-906-393A-9

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
|||
Db 3 AKK 5

RESULT 44

US-09-134-793-2

; Sequence 2, Application US/09134793
; Publication No. US20030040038A1
; GENERAL INFORMATION:
; APPLICANT: Dowdy, Steven F.
; APPLICANT: Jessee, Joel A.
; TITLE OF INVENTION: INDUCIBLE REGULATORY SYSTEM
; TITLE OF INVENTION: AND USE THEREOF
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/134,793
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/056,713
; FILING DATE: 22-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Corless, Peter F
; REGISTRATION NUMBER: 33,860
; REFERENCE/DOCKET NUMBER: 47275
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: protein
US-09-134-793-2

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7
|||
Db 7 RQR 9

RESULT 45

US-09-882-291-43

; Sequence 43, Application US/09882291
; Publication No. US20030040472A1
; GENERAL INFORMATION:
; APPLICANT: Zealand Pharmaceuticals A/S
; TITLE OF INVENTION: No. US20030040472A1el Peptide Conjugates
; FILE REFERENCE: 007-2001
; CURRENT APPLICATION NUMBER: US/09/882,291
; CURRENT FILING DATE: 2001-06-15
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide
sequence
US-09-882-291-43

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7
|||
Db 7 RQR 9

RESULT 46

US-09-775-052-2

; Sequence 2, Application US/09775052
; Publication No. US20030054000A1
; GENERAL INFORMATION:
; APPLICANT: Dowdy, Steven F.
; TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF
; FILE REFERENCE: 48881/1742
; CURRENT APPLICATION NUMBER: US/09/775,052
; CURRENT FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 09/208,966
; PRIOR FILING DATE: 1998-12-10
; PRIOR APPLICATION NUMBER: 60/082,402
; PRIOR FILING DATE: 1998-04-20
; PRIOR APPLICATION NUMBER: 60/069,012

; PRIOR FILING DATE: 1997-12-10
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 11
; TYPE: PRT
; ORGANISM: human
US-09-775-052-2

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7
|||
Db 7 RQR 9

RESULT 47

US-09-775-052-16
; Sequence 16, Application US/09775052
; Publication No. US20030054000A1
; GENERAL INFORMATION:
; APPLICANT: Dowdy, Steven F.
; TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF
; FILE REFERENCE: 48881/1742
; CURRENT APPLICATION NUMBER: US/09/775,052
; CURRENT FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 09/208,966
; PRIOR FILING DATE: 1998-12-10
; PRIOR APPLICATION NUMBER: 60/082,402
; PRIOR FILING DATE: 1998-04-20
; PRIOR APPLICATION NUMBER: 60/069,012
; PRIOR FILING DATE: 1997-12-10
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 11
; TYPE: PRT
; ORGANISM: human
US-09-775-052-16

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7
|||
Db 6 RQR 8

RESULT 48

US-09-775-052-52
; Sequence 52, Application US/09775052
; Publication No. US20030054000A1
; GENERAL INFORMATION:
; APPLICANT: Dowdy, Steven F.


```
; TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF
; FILE REFERENCE: 48881/1742
; CURRENT APPLICATION NUMBER: US/09/775,052
; CURRENT FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 09/208,966
; PRIOR FILING DATE: 1998-12-10
; PRIOR APPLICATION NUMBER: 60/082,402
; PRIOR FILING DATE: 1998-04-20
; PRIOR APPLICATION NUMBER: 60/069,012
; PRIOR FILING DATE: 1997-12-10
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 52
; LENGTH: 11
; TYPE: PRT
; ORGANISM: human
US-09-775-052-52
```

```
Query Match          27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy          5 RQR 7
             |||
Db          7 RQR 9
```

RESULT 49

```
US-09-847-946A-124
; Sequence 124, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 124
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:membrane
; OTHER INFORMATION: translocation domain
US-09-847-946A-124
```

```
Query Match          27.3%; Score 3; DB 10; Length 11;
```

Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7
|||
Db 7 RQR 9

RESULT 50

US-09-847-946A-125

; Sequence 125, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 125
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:membrane
; OTHER INFORMATION: translocation domain

US-09-847-946A-125

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7
|||
Db 7 RQR 9

RESULT 51

US-09-876-904A-5

; Sequence 5, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND
THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC
PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES

```
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusogenic/NLS peptide
; OTHER INFORMATION: conjugate from TAT of HIV
US-09-876-904A-5
```

```
Query Match          27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy          5 RQR 7
            |||
Db          7 RQR 9
```

RESULT 52

```
US-09-876-904A-10
; Sequence 10, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND
THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC
PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic fusogenic
; OTHER INFORMATION: peptide of TAT
US-09-876-904A-10
```

```
Query Match          27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy          5 RQR 7
```

Db |||
 7 RQR 9

RESULT 53

US-09-876-904A-50

; Sequence 50, Application US/09876904A

; Publication No. US20030072794A1

; GENERAL INFORMATION:

; APPLICANT: BOULIKAS, TENI

; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND
THERAPEUTIC

; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC
PEPTIDE

; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES

; FILE REFERENCE: TB-2002.00

; CURRENT APPLICATION NUMBER: US/09/876,904A

; CURRENT FILING DATE: 2001-06-08

; PRIOR APPLICATION NUMBER: US 60/210,925

; PRIOR FILING DATE: 2000-06-09

; NUMBER OF SEQ ID NOS: 629

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 50

; LENGTH: 11

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Human c-myc

; OTHER INFORMATION: oncoprotein

US-09-876-904A-50

Query Match 27.3%; Score 3; DB 10; Length 11;

Best Local Similarity 100.0%; Pred. No. 8.3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7

|||

Db 1 RQR 3

RESULT 54

US-09-876-904A-111

; Sequence 111, Application US/09876904A

; Publication No. US20030072794A1

; GENERAL INFORMATION:

; APPLICANT: BOULIKAS, TENI

; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND
THERAPEUTIC

; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC
PEPTIDE

; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES

; FILE REFERENCE: TB-2002.00

; CURRENT APPLICATION NUMBER: US/09/876,904A

; CURRENT FILING DATE: 2001-06-08

; PRIOR APPLICATION NUMBER: US 60/210,925

; PRIOR FILING DATE: 2000-06-09

; NUMBER OF SEQ ID NOS: 629

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 111
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HIV Tat
protein
US-09-876-904A-111

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7
|||
Db 6 RQR 8

RESULT 55
US-09-876-904A-200
; Sequence 200, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND
THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC
PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 200
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; OTHER INFORMATION: Karyophilic peptide
US-09-876-904A-200

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
|||
Db 3 AKK 5

RESULT 56
US-09-876-904A-232
; Sequence 232, Application US/09876904A

```
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND
THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC
PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 232
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Hydrophilic protein
US-09-876-904A-232
```

```
Query Match          27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy          7 RKD 9
            |||
Db          8 RKD 10
```

```
RESULT 57
US-09-876-904A-237
; Sequence 237, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND
THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC
PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 237
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Hydrophilic protein
US-09-876-904A-237
```

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKE 4
|||
Db 7 KKE 9

RESULT 58

US-09-876-904A-273
; Sequence 273, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND
THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC
PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 273
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Drosophila sp.
; FEATURE:
; OTHER INFORMATION: Recombination repair protein 1
US-09-876-904A-273

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKE 4
|||
Db 7 KKE 9

RESULT 59

US-09-876-904A-354
; Sequence 354, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND
THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC
PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00

```

; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 354
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human ATF-3 (in basic region that binds DNA)
US-09-876-904A-354

```

```

Query Match          27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      2 KKE 4
        |||
Db      7 KKE 9

```

RESULT 60

```

US-09-876-904A-434
; Sequence 434, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND
THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC
PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 434
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Drosophila sp.
; FEATURE:
; OTHER INFORMATION: Drosophila ultrabiothorax protein (from the
; OTHER INFORMATION: conserved 61 amino acid homeodomain segment only).
US-09-876-904A-434

```

```

Query Match          27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      2 KKE 4
        |||
Db      8 KKE 10

```


RESULT 61

US-09-876-904A-591

; Sequence 591, Application US/09876904A
 ; Publication No. US20030072794A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BOULIKAS, TENI
 ; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
 ; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
 ; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
 ; FILE REFERENCE: TB-2002.00
 ; CURRENT APPLICATION NUMBER: US/09/876,904A
 ; CURRENT FILING DATE: 2001-06-08
 ; PRIOR APPLICATION NUMBER: US 60/210,925
 ; PRIOR FILING DATE: 2000-06-09
 ; NUMBER OF SEQ ID NOS: 629
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 591
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Unknown Organism
 ; FEATURE:
 ; OTHER INFORMATION: Description of Unknown Organism: Trout testis H1 (194 aa).
 US-09-876-904A-591

Query Match 27.3%; Score 3; DB 10; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
 |||
 Db 1 AKK 3

RESULT 62

US-09-876-904A-597

; Sequence 597, Application US/09876904A
 ; Publication No. US20030072794A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BOULIKAS, TENI
 ; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
 ; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
 ; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
 ; FILE REFERENCE: TB-2002.00
 ; CURRENT APPLICATION NUMBER: US/09/876,904A
 ; CURRENT FILING DATE: 2001-06-08
 ; PRIOR APPLICATION NUMBER: US 60/210,925
 ; PRIOR FILING DATE: 2000-06-09
 ; NUMBER OF SEQ ID NOS: 629
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 597

; LENGTH: 11
; TYPE: PRT
; ORGANISM: Parechinus angulosus
; FEATURE:
; OTHER INFORMATION: Sea urchin Parechinus angulosus sperm H1 (248 aa).
US-09-876-904A-597

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
|||
Db 1 AKK 3

RESULT 63

US-09-820-053A-113
; Sequence 113, Application US/09820053A
; Publication No. US20030083243A1
; GENERAL INFORMATION:
; APPLICANT: Owen, Donald R.
; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
; FILE REFERENCE: HELX027
; CURRENT APPLICATION NUMBER: US/09/820,053A
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 113
; LENGTH: 11
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC SEQUENCE
; NAME/KEY: MOD_RES
; LOCATION: (11)
; OTHER INFORMATION: AMIDATION
US-09-820-053A-113

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
|||
Db 9 AKK 11

RESULT 64

US-09-820-053A-139
; Sequence 139, Application US/09820053A
; Publication No. US20030083243A1
; GENERAL INFORMATION:
; APPLICANT: Owen, Donald R.
; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
; FILE REFERENCE: HELX027
; CURRENT APPLICATION NUMBER: US/09/820,053A

```
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 139
; LENGTH: 11
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC SEQUENCE
; NAME/KEY: MOD_RES
; LOCATION: (11)
; OTHER INFORMATION: AMIDATION
US-09-820-053A-139
```

```
Query Match          27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy      1 AKK 3
        |||
Db      8 AKK 10
```

RESULT 65

```
US-09-845-612B-20
; Sequence 20, Application US/09845612B
; Publication No. US20030083261A1
; GENERAL INFORMATION:
; APPLICANT: YU, HONGTAO
; APPLICANT: TANG, ZHANYUN
; APPLICANT: LUO, XUELIAN
; APPLICANT: RIZO-REY, JOSE
; TITLE OF INVENTION: A CLASS OF 12MER PEPTIDES THAT INHIBIT THE FUNCTION OF
THE MITOTIC CHECK
; TITLE OF INVENTION: POINT PROTEIN MAD2
; FILE REFERENCE: UTSD:795
; CURRENT APPLICATION NUMBER: US/09/845,612B
; CURRENT FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 11
; TYPE: PRT
; ORGANISM: HIV-TAT PROTEIN
US-09-845-612B-20
```

```
Query Match          27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy      5 RQR 7
        |||
Db      7 RQR 9
```

RESULT 66

US-09-992-665-55

```
; Sequence 55, Application US/09992665
; Publication No. US20030092009A1
; GENERAL INFORMATION:
; APPLICANT: Kaia Palm
; TITLE OF INVENTION: PROFILING TUMOR SPECIFIC MARKERS FOR THE
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: CEMINES.002A
; CURRENT APPLICATION NUMBER: US/09/992,665
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 60/249,508
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe
US-09-992-665-55
```

```
Query Match          27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy          8 KDT 10
            |||
Db          3 KDT 5
```

```
RESULT 67
US-09-865-548A-35
; Sequence 35, Application US/09865548A
; Publication No. US20030096298A1
; GENERAL INFORMATION:
; APPLICANT: Barnea, Eilon
; APPLICANT: Beer, Ilan
; APPLICANT: Ziv, Tamar
; APPLICANT: Admon, Arie
; TITLE OF INVENTION: METHOD OF IDENTIFYING PEPTIDES CAPABLE OF BINDING TO MHC
MOLECULES,
; TITLE OF INVENTION: PEPTIDES IDENTIFIED THEREBY AND THEIR USES
; FILE REFERENCE: 01/22080
; CURRENT APPLICATION NUMBER: US/09/865,548A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: US 60/290,958
; PRIOR FILING DATE: 2001-05-16
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-865-548A-35
```

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KER 5
|||
Db 4 KER 6

RESULT 68

US-09-997-465B-2

; Sequence 2, Application US/09997465B

; Publication No. US20030118610A1

; GENERAL INFORMATION:

; APPLICANT: Stern, William

; APPLICANT: Mehta, No. US20030118610A1er M.

; APPLICANT: Ray, Martha V.L.

; TITLE OF INVENTION: IMPROVED ORAL DELIVERY OF PEPTIDES USING ENZYME-CLEAVABLE
MEMBRANE

; TITLE OF INVENTION: TRANSLOCATORS

; FILE REFERENCE: P/546-247

; CURRENT APPLICATION NUMBER: US/09/997,465B

; CURRENT FILING DATE: 2001-11-29

; NUMBER OF SEQ ID NOS: 22

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 2

; LENGTH: 11

; TYPE: PRT

; ORGANISM: Human immunodeficiency virus type 1

US-09-997-465B-2

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7
|||
Db 7 RQR 9

RESULT 69

US-09-997-465B-18

; Sequence 18, Application US/09997465B

; Publication No. US20030118610A1

; GENERAL INFORMATION:

; APPLICANT: Stern, William

; APPLICANT: Mehta, No. US20030118610A1er M.

; APPLICANT: Ray, Martha V.L.

; TITLE OF INVENTION: IMPROVED ORAL DELIVERY OF PEPTIDES USING ENZYME-CLEAVABLE
MEMBRANE

; TITLE OF INVENTION: TRANSLOCATORS

; FILE REFERENCE: P/546-247

; CURRENT APPLICATION NUMBER: US/09/997,465B

; CURRENT FILING DATE: 2001-11-29

; NUMBER OF SEQ ID NOS: 22

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 18

; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-997-465B-18

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7
|||
Db 7 RQR 9

RESULT 70

US-09-911-261A-18
; Sequence 18, Application US/09911261A
; Publication No. US20030134350A1
; GENERAL INFORMATION:
; APPLICANT: Sera, Takashi
; TITLE OF INVENTION: Zinc Finger Domain Recognition Code and Uses Thereof
; FILE REFERENCE: 109845.135
; CURRENT APPLICATION NUMBER: US/09/911,261A
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/220,060
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-09-911-261A-18

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7
|||
Db 7 RQR 9

RESULT 71

US-09-798-053-10
; Sequence 10, Application US/09798053
; Publication No. US20030158378A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Ke
; APPLICANT: Cam, Linh
; APPLICANT: Nakayama, Naoki
; TITLE OF INVENTION: Chordin-Like-2 Molecules and Uses Thereof
; FILE REFERENCE: 01-005
; CURRENT APPLICATION NUMBER: US/09/798,053
; CURRENT FILING DATE: 2003-03-25
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 10
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-798-053-10

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7
|||
Db 7 RQR 9

RESULT 72

US-09-854-248-20
; Sequence 20, Application US/09854248
; Publication No. US20030175247A1
; GENERAL INFORMATION:
; APPLICANT: Salgaller, Michael L.
; APPLICANT: Boynton, Alton L.
; TITLE OF INVENTION: METHOD TO INCREASE CLASS I PRESENTATION OF EXOGENOUS
; TITLE OF INVENTION: ANTIGENS BY HUMAN DENDRITIC CELLS
; FILE REFERENCE: 20093-8-1US
; CURRENT APPLICATION NUMBER: US/09/854,248
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/203,758
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-248-20

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKE 4
|||
Db 9 KKE 11

RESULT 73

US-09-962-756-1790
; Sequence 1790, Application US/09962756
; Publication No. US20030195147A1
; GENERAL INFORMATION:
; APPLICANT: PILLUTLA, RENUKA
; APPLICANT: BRISSETTE, RENEE
; APPLICANT: BLUME, ARTHUR J.
; APPLICANT: SCHAFFER, LAUGE
; APPLICANT: BRANDT, JAKOB
; APPLICANT: GOLDSTEIN, NEIL I.

```

; APPLICANT: SPETZLER, JANE
; APPLICANT: OSTERGAARD, SOREN
; APPLICANT: HANSEN, PER HERTZ
; TITLE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS
; FILE REFERENCE: 1878-4051US1
; CURRENT APPLICATION NUMBER: US/09/962,756
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/538,038
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/146,127
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 2227
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1790
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-962-756-1790

```

```

Query Match          27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy          4 ERQ 6
            |||
Db          8 ERQ 10

```

RESULT 74

```

US-09-962-756-2008
; Sequence 2008, Application US/09962756
; Publication No. US20030195147A1
; GENERAL INFORMATION:
; APPLICANT: PILLUTLA, RENUKA
; APPLICANT: BRISSETTE, RENEE
; APPLICANT: BLUME, ARTHUR J.
; APPLICANT: SCHAFFER, LAUGE
; APPLICANT: BRANDT, JAKOB
; APPLICANT: GOLDSTEIN, NEIL I.
; APPLICANT: SPETZLER, JANE
; APPLICANT: OSTERGAARD, SOREN
; APPLICANT: HANSEN, PER HERTZ
; TITLE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS
; FILE REFERENCE: 1878-4051US1
; CURRENT APPLICATION NUMBER: US/09/962,756
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/538,038
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/146,127
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 2227
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2008
; LENGTH: 11

```


; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-962-756-2008

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ERQ 6
|||
Db 7 ERQ 9

RESULT 75

US-09-784-553C-50
; Sequence 50, Application US/09784553C
; Publication No. US20040043378A1
; GENERAL INFORMATION:
; APPLICANT: ZHOU, MING-MING
; APPLICANT: AGGARWAL, ANEEL
; TITLE OF INVENTION: METHODS OF IDENTIFYING MODULATORS OF BROMODOMAINS
; FILE REFERENCE: 2459-1-003 CIP
; CURRENT APPLICATION NUMBER: US/09/784,553C
; CURRENT FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: 09/510,314
; PRIOR FILING DATE: 2000-02-22
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 50
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic HIV-1 Tat peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (5)..(5)
; OTHER INFORMATION: acetylated lysine
US-09-784-553C-50

Query Match 27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7
|||
Db 8 RQR 10

Search completed: April 8, 2004, 16:35:33
Job time : 31.3077 secs

OM protein - protein search, using sw model

Run on: April 8, 2004, 15:30:07 ; Search time 27.7692 Seconds
(without alignments)
124.984 Million cell updates/sec

Title: US-09-787-443A-2
Perfect score: 11
Sequence: 1 AKKERQRKDTQ 11

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size : 0

Total number of hits satisfying chosen parameters: 460

Minimum DB seq length: 11
Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

Database : SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%
Result Query
No. Score Match Length DB ID Description

1	4	36.4	11	4	Q9Y3G2	Q9y3g2 homo sapien
2	4	36.4	11	15	Q9DYW4	Q9dyw4 human immun
3	3	27.3	11	4	Q9H4H5	Q9h4h5 homo sapien
4	3	27.3	11	6	Q9TRW5	Q9trw5 bos taurus
5	2	18.2	11	2	Q9R790	Q9r790 borrelia ga
6	2	18.2	11	2	Q9L4F7	Q9l4f7 bacillus ce
7	2	18.2	11	2	Q47606	Q47606 escherichia
8	2	18.2	11	2	Q9R4B1	Q9r4b1 streptococc
9	2	18.2	11	2	Q9S618	Q9s618 prochloroco
10	2	18.2	11	2	Q9R5P3	Q9r5p3 serratia ma
11	2	18.2	11	2	Q9EUZ3	Q9euz3 escherichia
12	2	18.2	11	2	Q8RMI8	Q8rmi8 enterococcu
13	2	18.2	11	2	Q9RBV0	Q9rbv0 pseudomonas
14	2	18.2	11	2	Q9K332	Q9k332 staphylococ
15	2	18.2	11	2	Q9RFZ2	Q9rfz2 mycoplasma
16	2	18.2	11	2	P95518	P95518 pasteurella
17	2	18.2	11	2	Q47420	Q47420 escherichia
18	2	18.2	11	2	Q44090	Q44090 acholeplasm
19	2	18.2	11	2	Q56413	Q56413 escherichia
20	2	18.2	11	2	Q9R446	Q9r446 neisseria g
21	2	18.2	11	2	Q91UY9	Q9luy9 escherichia
22	2	18.2	11	2	Q8GMU3	Q8gmu3 acinetobact
23	2	18.2	11	3	Q9UR95	Q9ur95 pichia angu
24	2	18.2	11	3	Q9HFN8	Q9hfn8 candida rug
25	2	18.2	11	4	Q14759	Q14759 homo sapien
26	2	18.2	11	4	Q16427	Q16427 homo sapien
27	2	18.2	11	4	O60761	O60761 homo sapien
28	2	18.2	11	4	O94785	O94785 homo sapien
29	2	18.2	11	4	Q8NI03	Q8ni03 homo sapien
30	2	18.2	11	5	Q9UAR8	Q9uar8 aedes aegyp
31	2	18.2	11	5	Q9TWX6	Q9twx6 manduca sex
32	2	18.2	11	5	Q99292	Q99292 drosophila
33	2	18.2	11	5	Q8MM58	Q8mm58 heliconius
34	2	18.2	11	5	Q86D32	Q86d32 trypanosoma
35	2	18.2	11	5	Q86D31	Q86d31 trypanosoma
36	2	18.2	11	5	Q95PX6	Q95px6 caenorhabdi
37	2	18.2	11	7	Q9UEX7	Q9uex7 homo sapien
38	2	18.2	11	7	O77911	O77911 oreochromis
39	2	18.2	11	8	Q8MEL7	Q8mel7 sida hooker
40	2	18.2	11	8	Q8MAZ1	Q8maz1 maripa pani
41	2	18.2	11	8	Q8MB39	Q8mb39 wilsonia hu
42	2	18.2	11	8	Q8MEM2	Q8mem2 lagunaria p
43	2	18.2	11	8	Q8MB58	Q8mb58 seddera hir
44	2	18.2	11	8	Q8MAZ3	Q8maz3 maripa repe
45	2	18.2	11	8	Q8MES5	Q8mes5 abelmoschus
46	2	18.2	11	8	Q8MEP0	Q8mep0 hibiscus pe
47	2	18.2	11	8	Q8MES1	Q8mes1 alyogyne pi
48	2	18.2	11	8	Q8MEP3	Q8mep3 hibiscus no
49	2	18.2	11	8	Q8MBE1	Q8mbe1 ipomoea alb
50	2	18.2	11	8	Q8MEQ7	Q8meq7 hibiscus dr
51	2	18.2	11	8	Q35374	Q35374 paramecium
52	2	18.2	11	8	Q8MEL9	Q8mel9 pavonia has
53	2	18.2	11	8	Q8MB77	Q8mb77 odonellia h
54	2	18.2	11	8	Q8MER0	Q8mer0 hibiscus co
55	2	18.2	11	8	Q8MES3	Q8mes3 alyogyne cr
56	2	18.2	11	8	Q8MB79	Q8mb79 aniseia arg
57	2	18.2	11	8	Q8MB97	Q8mb97 merremia pe

58	2	18.2	11	8	Q8MEP5	Q8mep5 hibiscus mi
59	2	18.2	11	8	Q8MER1	Q8mer1 hibiscus ca
60	2	18.2	11	8	Q8MER7	Q8mer7 fioria viti
61	2	18.2	11	9	Q38415	Q38415 bacteriopha
62	2	18.2	11	9	Q37925	Q37925 bacteriopha
63	2	18.2	11	10	Q9S8X4	Q9s8x4 glycine max
64	2	18.2	11	10	Q39784	Q39784 gossypium h
65	2	18.2	11	10	O82070	O82070 triticum ae
66	2	18.2	11	10	Q04131	Q04131 lycopersico
67	2	18.2	11	10	P83092	P83092 spinacia ol
68	2	18.2	11	11	P97755	P97755 rattus norv
69	2	18.2	11	11	Q99N81	Q99n81 mus musculu
70	2	18.2	11	11	Q9JLE6	Q9jle6 rattus norv
71	2	18.2	11	11	Q8R2J7	Q8r2j7 mesocricetu
72	2	18.2	11	12	P89269	P89269 xestia c-ni
73	2	18.2	11	12	Q84073	Q84073 influenzavi
74	2	18.2	11	12	Q69269	Q69269 equine herp
75	2	18.2	11	13	Q800X7	Q800x7 chelydra se
76	2	18.2	11	13	Q7T285	Q7t285 geochelone
77	2	18.2	11	13	Q7T284	Q7t284 geochelone
78	2	18.2	11	13	Q7T283	Q7t283 geochelone
79	2	18.2	11	13	Q7SX72	Q7sx72 geochelone
80	2	18.2	11	13	Q7SX71	Q7sx71 geochelone
81	2	18.2	11	15	Q9DZ32	Q9dz32 human immun
82	2	18.2	11	16	Q9K7A4	Q9k7a4 bacillus ha
83	1	9.1	11	2	Q9AIY6	Q9aiy6 carsonella
84	1	9.1	11	2	O68237	O68237 borrelia bu
85	1	9.1	11	2	Q48933	Q48933 mycobacteri
86	1	9.1	11	2	Q47451	Q47451 escherichia
87	1	9.1	11	2	Q9AIZ7	Q9aiz7 carsonella
88	1	9.1	11	2	Q8RKN1	Q8rkn1 escherichia
89	1	9.1	11	2	Q52526	Q52526 rhizobium s
90	1	9.1	11	2	Q8KHL0	Q8khl0 streptococc
91	1	9.1	11	2	Q47602	Q47602 escherichia
92	1	9.1	11	2	Q8L2T4	Q8l2t4 neisseria m
93	1	9.1	11	2	Q9R7U8	Q9r7u8 pseudomonas
94	1	9.1	11	2	Q9S623	Q9s623 prochloroco
95	1	9.1	11	2	P77404	P77404 escherichia
96	1	9.1	11	2	Q9RQ60	Q9rq60 buchnera ap
97	1	9.1	11	2	P96319	P96319 desulfovibr
98	1	9.1	11	2	Q93RM6	Q93rm6 staphylococ
99	1	9.1	11	2	Q47600	Q47600 escherichia
100	1	9.1	11	2	O87882	O87882 mycobacteri

ALIGNMENTS

RESULT 1

Q9Y3G2

ID Q9Y3G2 PRELIMINARY; PRT; 11 AA.

AC Q9Y3G2;

DT 01-NOV-1999 (TrEMBLrel. 12, Created)

DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE LSFR2 protein (Fragment).

GN LSFR2.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99299247; PubMed=10369878;
 RA Gilley J., Fried M.;
 RT "Extensive gene order differences within regions of conserved synteny
 RT between the Fugu and human genomes: implications for chromosomal
 RT evolution and the cloning of disease genes.";
 RL Hum. Mol. Genet. 8:1313-1320(1999).
 DR EMBL; Y17456; CAB44349.1; -.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1342 MW; 68C5E5D7A8772324 CRC64;

Query Match 36.4%; Score 4; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 7.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQRK 8
 ||||
 Db 2 RQRK 5

RESULT 2

Q9DYW4

ID Q9DYW4 PRELIMINARY; PRT; 11 AA.
 AC Q9DYW4;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Gag polyprotein (Fragment).
 GN GAG.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20461476; PubMed=11005867;
 RA Martinez-Picado J., DePasquale M.P., Kartsonis N., Hanna G.J.,
 RA Wong J., Finzi D., Rosenberg E., Gunthard H.F., Sutton L., Savara A.,
 RA Petropoulos C.J., Hellmann N., Walker B.D., Richman D.D.,
 RA Siliciano R., D'Aquila R.T.;
 RT "Antiretroviral resistance during successful therapy of HIV type 1
 RT infection.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:10948-10953(2000).
 DR EMBL; AF292846; AAG25476.1; -.
 KW Polyprotein.
 FT NON_TER 1 1
 SQ SEQUENCE 11 AA; 1202 MW; 02F874A6240AB2C4 CRC64;

Query Match 36.4%; Score 4; DB 15; Length 11;
 Best Local Similarity 100.0%; Pred. No. 7.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RKDT 10
 ||||
Db 7 RKDT 10

RESULT 3

Q9H4H5

ID Q9H4H5 PRELIMINARY; PRT; 11 AA.
AC Q9H4H5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE DJ661I20.2 (Novel helicase C-terminal domain and SNF2 N-terminal
DE domains containing protein) (Fragment).
GN DJ620E11.1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Skuce C.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AL031669; CAC17164.2; -.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1420 MW; 5EB2C32A3326D053 CRC64;

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKE 4
 |||
Db 7 KKE 9

RESULT 4

Q9TRW5

ID Q9TRW5 PRELIMINARY; PRT; 11 AA.
AC Q9TRW5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE 25 kDa protein P25, peptide F4 (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=91372400; PubMed=1909972;
RA Takahashi M., Tomizawa K., Ishiguro K., Sato K., Omori A., Sato S.,
RA Shiratsuchi A., Uchida T., Imahori K.;
RT "A novel brain-specific 25 kDa protein (p25) is phosphorylated by a
RT Ser/Thr-Pro kinase (TPK II) from tau protein kinase fractions.";

RL FEBS Lett. 289:37-43(1991).

FT NON_TER 1 1

FT NON_TER 11 11

SQ SEQUENCE 11 AA; 1276 MW; CAF72DAF65A76AA9 CRC64;

Query Match 27.3%; Score 3; DB 6; Length 11;

Best Local Similarity 100.0%; Pred. No. 8.8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KER 5

|||

Db 1 KER 3

RESULT 5

Q9R790

ID Q9R790 PRELIMINARY; PRT; 11 AA.

AC Q9R790;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Outer surface protein C (Fragment).

GN OSPC.

OS Borrelia garinii.

OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.

OX NCBI_TaxID=29519;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=G25;

RX MEDLINE=97426044; PubMed=9282748;

RA Tilly K., Casjens S., Stevenson B., Bono J.L., Samuels D.S., Hogan D.,

RA Rosa P.;

RT "he Borrelia burgdorferi circular plasmid cp26: conservation of

RT plasmid structure and targeted inactivation of the ospC gene.";

RL Mol. Microbiol. 25:361-374(1997).

DR EMBL; U93700; AAC45535.1; -.

DR GO; GO:0009279; C:external outer membrane (sensu Gram-negativ. . .; IEA.

DR GO; GO:0003793; F:defense/immunity protein activity; IEA.

DR GO; GO:0006952; P:defense response; IEA.

DR InterPro; IPR001800; Lipoprotein_6.

DR Pfam; PF01441; Lipoprotein_6; 1.

FT NON_TER 11 11

SQ SEQUENCE 11 AA; 1250 MW; 0868D864C5B731A4 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 1e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KK 3

||

Db 2 KK 3

RESULT 6

Q9L4F7

ID Q9L4F7 PRELIMINARY; PRT; 11 AA.

AC Q9L4F7;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE Phosphatidylinositol-specific phospholipase C (PI-PLC)
 DE (Fragment).
 GN PLCA.
 OS Bacillus cereus.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1396;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 14579 type strain;
 RX MEDLINE=20055637; PubMed=10589720;
 RA Okstad O., Gominet M., Purnelle B., Rose M., Lereclus D., Kolsto A.B.;
 RT "Sequence analysis of three Bacillus cereus loci under P1cR-regulated
 RT genes encoding degradative enzymes and enterotoxin."
 RL Microbiology 145:3129-3138(1999).
 DR EMBL; AJ243711; CAB69804.1; -.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1335 MW; 4277A30E20572333 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KK 3
 ||
 Db 4 KK 5

RESULT 7

Q47606
 ID Q47606 PRELIMINARY; PRT; 11 AA.
 AC Q47606;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE REase protein (Fragment).
 GN REASE.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91139577; PubMed=1995588;
 RA Tao T., Bourne J.C., Blumenthal R.M.;
 RT "A family of regulatory genes associated with type II restriction-
 RT modification systems."
 RL J. Bacteriol. 173:1367-1375(1991).
 DR EMBL; M63622; AAA24562.1; -.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1370 MW; 68C1FF9959CB133B CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KE 4
||
Db 5 KE 6

RESULT 8

Q9R4B1

ID Q9R4B1 PRELIMINARY; PRT; 11 AA.
AC Q9R4B1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE BX protein (Fragment).
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE.
RX MEDLINE=95252678; PubMed=7734831;
RA Gerlach D., Gunther E., Kohler W., Vettermann S., Fleischer B.,
RA Schmidt K.H.;
RT "Isolation and characterization of a mitogen characteristic of group A
streptococci (Streptococcus pyogenes).";
RL Int. J. Med. Microbiol. Virol. Parasitol. Infect. Dis. 282:67-
RL 82(1995).
SQ SEQUENCE 11 AA; 1216 MW; CE527287CAA455A2 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 TQ 11
||
Db 2 TQ 3

RESULT 9

Q9S618

ID Q9S618 PRELIMINARY; PRT; 11 AA.
AC Q9S618;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Cytochrome b6/f complex subunit IV (Fragment).
GN PETD.
OS Prochlorococcus sp.
OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=1220;
RN [1]
RP SEQUENCE FROM N.A.
RA Urbach E., Chisholm S.W.;
RT "Genetic diversity in Prochlorococcus populations flow cytometrically
sorted from the Sargasso Sea and Gulf Stream.";
RL Limnol. Oceanogr. 43:1615-1630(1998).

DR EMBL; AF070132; AAD20740.1; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1297 MW; 5CC38013B7633337 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KK 3
||
Db 5 KK 6

RESULT 10

Q9R5P3

ID Q9R5P3 PRELIMINARY; PRT; 11 AA.
AC Q9R5P3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE SM2=NUCLEASE (Fragment).
OS *Serratia marcescens*.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; *Serratia*.
OX NCBI_TaxID=615;
RN [1]
RP SEQUENCE.
RX MEDLINE=92134331; PubMed=1663739;
RA Bannikova G.E., Blagova E.V., Dementiev A.A., Morgunova E.Yu.,
RA Mikchailov A.M., Shlyapnikov S.V., Varlamov V.P., Vainshtein B.K.;
RT "Two isoforms of *Serratia marcescens* nuclease. Crystallization and
RT preliminary X-ray investigation of the enzyme."
RL Biochem. Int. 24:813-822(1991).
DR PIR; A27356; A27356.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1179 MW; 6DF18EE04AA045BB CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 DT 10
||
Db 1 DT 2

RESULT 11

Q9EUZ3

ID Q9EUZ3 PRELIMINARY; PRT; 11 AA.
AC Q9EUZ3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Ribosome binding factor A (Fragment).
GN RBFA.
OS *Escherichia coli*.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IQ490;
 RA Hedegaard J., Kristensen J.E., Nakamura Y., Sperling-Petersen H.U.,
 RA Mortensen K.K.;
 RT "Sequence of the infB gene from Escherichia coli strain IQ489 and
 RT IQ490."
 RL Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AJ132862; CAC20133.1; -.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1319 MW; 6B234CFE740879CB CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2
 ||
 Db 2 AK 3

RESULT 12

Q8RMI8

ID Q8RMI8 PRELIMINARY; PRT; 11 AA.
 AC Q8RMI8;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE ErmB (Fragment).
 GN ERMB.
 OS Enterococcus hirae.
 OG Plasmid pMKH1.
 OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
 OX NCBI_TaxID=1354;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Borgen K., Sorum M., Wasteson Y., Kruse H., Oppegaard H.;
 RT "Genetic linkage between ermB and vanA in Enterococcus hirae of
 RT poultry origin."
 RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF493942; AAM18554.1; -.
 DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
 KW Plasmid.
 FT NON_TER 1 1
 SQ SEQUENCE 11 AA; 1359 MW; 08A7A8AA49C7273B CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RK 8
 ||
 Db 10 RK 11

RESULT 13

Q9RBV0

ID Q9RBV0 PRELIMINARY; PRT; 11 AA.
 AC Q9RBV0;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Resolvase (Fragment).
 OS Pseudomonas sp. R9.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=101164;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=R9; TRANSPOSON=Tn1404;
 RX MEDLINE=20011227; PubMed=10543801;
 RA Schnabel E.L., Jones A.L.;
 RT "Distribution of tetracycline resistance genes and transposons among
 RT phylloplane bacteria in Michigan apple orchards."
 RL Appl. Environ. Microbiol. 65:4898-4907(1999).
 DR EMBL; AF157800; AAD48002.1; -.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1307 MW; D00B18E258704416 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QR 7
 ||
 Db 4 QR 5

RESULT 14

Q9K332

ID Q9K332 PRELIMINARY; PRT; 11 AA.
 AC Q9K332;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE Geh (Fragment).
 GN GEH.
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VARIOUS STRAINS;
 RX MEDLINE=20187516; PubMed=10722640;
 RA Cramton S.E., Schnell N.F., Gotz F., Bruckner R.;
 RT "Identification of a new repetitive element in Staphylococcus
 RT aureus."
 RL Infect. Immun. 68:2344-2348(2000).
 DR EMBL; AF195967; AAF60251.1; -.
 DR EMBL; AF195963; AAF60243.1; -.
 DR EMBL; AF195964; AAF60245.1; -.

DR EMBL; AF195965; AAF60247.1; -.
DR EMBL; AF195966; AAF60249.1; -.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1262 MW; 4F978F86AAB1A723 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 DT 10
||
Db 7 DT 8

RESULT 15

Q9RFZ2

ID Q9RFZ2 PRELIMINARY; PRT; 11 AA.
AC Q9RFZ2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Fructose biphosphate aldolase (Fragment).
GN FBA.
OS Mycoplasma mycoides subsp. capri.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=40477;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PG3;
RX MEDLINE=20193983; PubMed=10727835;
RA Thiaucourt F., Lorenzon S., David A., Breard A.;
RT "Phylogeny of the Mycoplasma mycoides cluster as shown by sequencing
RT of a putative membrane protein gene."
RL Vet. Microbiol. 72:251-268(2000).
DR EMBL; AF162998; AAF15255.1; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1371 MW; 50B0881A3331FB57 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KK 3
||
Db 7 KK 8

RESULT 16

P95518

ID P95518 PRELIMINARY; PRT; 11 AA.
AC P95518;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Ribosomal protein RpsA (Fragment).
GN RPSA.
OS Pasteurella haemolytica.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 OC Pasteurellaceae; Mannheimia.
 OX NCBI_TaxID=75985;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PHL101;
 RX MEDLINE=97164347; PubMed=9011038;
 RA Highlander S.K., Garza O., Brown B.J., Koby S., Oppenheim A.B.;
 RT "Isolation and characterization of the integration host factor genes
 RT of Pasteurella haemolytica.";
 RL FEMS Microbiol. Lett. 146:181-188(1997).
 DR EMBL; U56139; AAC44845.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 11 AA; 1168 MW; 7A4BFD38D339CDDDB CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2
 ||
 Db 8 AK 9

RESULT 17

Q47420

ID Q47420 PRELIMINARY; PRT; 11 AA.
 AC Q47420;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE ORF11 protein.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=92041688; PubMed=1657895;
 RA Sharples G.J., Lloyd R.G.;
 RT "Resolution of Holliday junctions in Escherichia coli: Identification
 RT of the ruvC gene product as a 19-Kilodalton protein.";
 RL J. Bacteriol. 173:7711-7715(1991).
 DR EMBL; X59551; CAA42127.1; -.
 DR PIR; S19015; S19015.
 SQ SEQUENCE 11 AA; 1215 MW; DD8D6D4D56C6D33D CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2
 ||
 Db 4 AK 5

RESULT 18

Q44090

ID Q44090 PRELIMINARY; PRT; 11 AA.
 AC Q44090;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical export segment (Fragment).
 OS Acholeplasma laidlawii.
 OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;
 OC Acholeplasmataceae; Acholeplasma.
 OX NCBI_TaxID=2148;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A-EF22;
 RA Boyer M.J., Jarhede T.K., Tegman V., Wieslander A.;
 RT "Sequence regions from Acholeplasma laidlawii which restore export of
 RT beta-lactamase in Escherichia coli.";
 RL Submitted (JUN-1993) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; Z22875; CAA80495.1; -.
 DR PIR; S33519; S33519.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1234 MW; 5C9D2AE8A682C337 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KK 3
 ||
 Db 2 KK 3

RESULT 19

Q56413

ID Q56413 PRELIMINARY; PRT; 11 AA.
 AC Q56413;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE IS602L region DNA, 5' end (Fragment).
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TRANSPOSON=Transposon Tn602;
 RX MEDLINE=87318208; PubMed=2819910;
 RA Stibitz S., Davies J.E.;
 RT "Tn602: A naturally occurring relative of Tn903 with direct repeats.";
 RL Plasmid 17:202-209(1987).
 DR EMBL; M22735; AAA27464.1; -.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1361 MW; 447E8354A05339C3 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2
||
Db 1 AK 2

RESULT 20

Q9R446

ID Q9R446 PRELIMINARY; PRT; 11 AA.
AC Q9R446;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Carbamoyl-phosphate synthase subunit A (Fragment).
GN CARA.
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=485;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MS11, and FA1090;
RX MEDLINE=95291461; PubMed=7773412;
RA Lawson F.S., Billowes F.M., Dillon J.A.;
RT "Organization of carbamoyl-phosphate synthase genes in Neisseria
RT gonorrhoeae includes a large, variable intergenic sequence which is
RT also present in other Neisseria species.";
RL Microbiology 141:0-0(0).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MS11, and FA1090;
RA Brinkman F.S.L., Francis F.M., Dillon J.R.;
RT "Complexity of the variable sequence between the carbamoyl-phosphate
RT synthase genes of Neisseria species.";
RL Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF029363; AAC78453.1; -.
DR EMBL; AF029362; AAC78452.1; -.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1178 MW; 0C07A8E3DDD33694 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2
||
Db 8 AK 9

RESULT 21

Q91UY9

ID Q91UY9 PRELIMINARY; PRT; 11 AA.
AC Q91UY9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Insertion site for insertion element IS903.B, upstream of kanamycin
 DE resistance gene (Fragment).
 OS *Escherichia coli*.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; *Escherichia*.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TRANSPOSON=Tn2680;
 RX MEDLINE=85234397; PubMed=2989253;
 RA Mollet B., Clerget M., Meyer J., Iida S.;
 RT "Organization of the Tn6-related kanamycin resistance transposon
 RT Tn2680 carrying two copies of IS26 and an IS903 variant, IS903.B.";
 RL J. Bacteriol. 163:55-60(1985).
 DR EMBL; M11420; AAA27427.1; -.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1278 MW; 03902598AB0416D0 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QR 7
 ||
 Db 5 QR 6

RESULT 22
 Q8GMU3

ID Q8GMU3 PRELIMINARY; PRT; 11 AA.
 AC Q8GMU3;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Putative catalase isozyme (Fragment).
 GN KATA.
 OS *Acinetobacter lwoffii*.
 OG Plasmid pKLH202.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Moraxellaceae; *Acinetobacter*.
 OX NCBI_TaxID=28090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TC108;
 RA Kholodii G.Y., Yurieva O.V., Mindlin S.Z., Gorlenko Z.M.,
 RA Nikiforov V.G.;
 RT "pKLH2-like aberrant transposons and possible mechanisms of their
 RT dissemination.";
 RL Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AJ250245; CAC80800.1; -.
 DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
 KW Plasmid.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1233 MW; 81A15757B333276A CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KK 3
||
Db 6 KK 7

RESULT 23

Q9UR95

ID Q9UR95 PRELIMINARY; PRT; 11 AA.
AC Q9UR95;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Heat shock protein 60 homolog (Fragment).
OS Pichia angusta (Yeast) (Hansenula polymorpha).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Pichia.
OX NCBI_TaxID=4905;
RN [1]
RP SEQUENCE.
RX MEDLINE=93223840; PubMed=8096822;
RA Evers M.E., Huhse B., Titorenko V.I., Kunau W.H., Hartl F.U.,
RA Harder W., Veenhuis M.;
RT "Affinity purification of molecular chaperones of the yeast Hansenula
RT polymorpha using immobilized denatured alcohol oxidase.";
RL FEBS Lett. 321:32-36(1993).
SQ SEQUENCE 11 AA; 1230 MW; 71872C1779C3372B CRC64;

Query Match 18.2%; Score 2; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KE 4
||
Db 3 KE 4

RESULT 24

Q9HFN8

ID Q9HFN8 PRELIMINARY; PRT; 11 AA.
AC Q9HFN8;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Acyl carrier protein (Fragment).
GN ACP.
OS Candida rugosa (Yeast) (Candida cylindracea).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5481;
RN [1]
RP SEQUENCE FROM N.A.
RA Biasio W.;
RL Thesis (2000), University of Vienna, Austria.

DR EMBL; AJ279021; CAC08812.1; -.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1274 MW; D2E4CC3976C40732 CRC64;

Query Match 18.2%; Score 2; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQ 6
||
Db 6 RQ 7

RESULT 25

Q14759

ID Q14759 PRELIMINARY; PRT; 11 AA.
AC Q14759;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Lymphocyte cytosolic protein 2 (Fragment).
GN LCP2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Sunden S.L.F., Carr L.L., Clements J.L, Motto D.G., Koretzky G.A.;
RT "Polymorphism in and localization of the gene encoding the 76 kDa SH2
RT domain-containing Leukocyte Protein (SLP-76) to chromosome 5q33.1-
RT qter.";
RL Genomics 0:0-0(1995).
DR EMBL; U44065; AAA93308.1; -.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1242 MW; D695104224072DDD CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RK 8
||
Db 7 RK 8

RESULT 26

Q16427

ID Q16427 PRELIMINARY; PRT; 11 AA.
AC Q16427;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE Dystrophin protein (Fragment).
GN DYSTROPHIN.
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96163501; PubMed=8566960;
 RA Holder E., Maeda M., Bies R.D.;
 RT "Expression and regulation of the dystrophin Purkinje promoter in
 RT human skeletal muscle, heart, and brain."
 RL Hum. Genet. 97:232-239(1996).
 DR EMBL; S81419; AAD14362.1; -.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1299 MW; DDCC84321AB5A5A2 CRC64;

 Query Match 18.2%; Score 2; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ER 5
 ||
 Db 8 ER 9

RESULT 27

O60761

ID O60761 PRELIMINARY; PRT; 11 AA.
 AC O60761;
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE NPT-1 protein (Fragment).
 GN NPT-1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98207718; PubMed=9545579;
 RA Taketani Y., Miyamoto K., Chikamori M., Tanaka K., Yamamoto H.,
 RA Tatsumi S., Morita K., Takeda E.;
 RT "Characterization of the 5' flanking region of the human NPT-1
 RT Na+/phosphate cotransporter gene."
 RL Biochim. Biophys. Acta 1396:267-272(1998).
 DR EMBL; D83236; BAA25645.1; -.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1358 MW; 884E2D4E6734044A CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KK 3
 ||
 Db 10 KK 11

RESULT 28

O94785

ID O94785 PRELIMINARY; PRT; 11 AA.
 AC O94785;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
 DE Thrombopoietin (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sasaki Y., Takahashi T., Nakamura K., Okuno Y., Nakao K.;
 RT "Production of Thrombopoietin by Human Carcinomas and Its Novel mRNA
 RT Isoforms."
 RL Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AB014683; BAA34932.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 11 AA; 1203 MW; 5FE19F44B6C1A877 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 TQ 11
 ||
 Db 6 TQ 7

RESULT 29

Q8NI03

ID Q8NI03 PRELIMINARY; PRT; 11 AA.
 AC Q8NI03;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE 25 hydroxyvitamin d3 1-alpha hydroxylase (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ebert R., Schneider D., Jovanovic M., Adamski J., Jakob F.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF500480; AAM21669.1; -.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1298 MW; 82C14E84CB533731 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 TQ 11
 ||

Db 2 TQ 3

RESULT 30

Q9UAR8

ID Q9UAR8 PRELIMINARY; PRT; 11 AA.
AC Q9UAR8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Sialokinin I preproprotein (Fragment).
OS Aedes aegypti (Yellowfever mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
OX NCBI_TaxID=7159;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Rockefeller/Red; TISSUE=Salivary gland;
RX MEDLINE=20099025; PubMed=10620041;
RA Beerntsen B.T., Champagne D.E., Coleman J.L., Campos Y.A., James A.A.;
RT "Characterization of the Sialokinin I gene encoding the salivary
RT vasodilator of the yellow fever mosquito, Aedes aegypti."
RL Insect Mol. Biol. 8:459-467(1999).
DR EMBL; AF108100; AAD16884.1; -.
DR GO; GO:0007268; P:synaptic transmission; IEA.
DR GO; GO:0007217; P:tachykinin signaling pathway; IEA.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR PROSITE; PS00267; TACHYKININ; 1.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1203 MW; 8BAD77C6B59C33A CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 DT 10
||
Db 1 DT 2

RESULT 31

Q9TWX6

ID Q9TWX6 PRELIMINARY; PRT; 11 AA.
AC Q9TWX6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Juvenile hormone binding protein, JHBP=12.5 kDa CNBR peptide
DE (Fragment).
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingioidea;
OC Sphingidae; Sphinginae; Manduca.
OX NCBI_TaxID=7130;
RN [1]
RP SEQUENCE.
RX MEDLINE=92134256; PubMed=1734862;

RA Touhara K., Prestwich G.D.;
 RT "Binding site mapping of a photoaffinity-labeled juvenile hormone
 RT binding protein.";
 RL Biochem. Biophys. Res. Commun. 182:466-473(1992).
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1071 MW; D232A98E705045BD CRC64;

 Query Match 18.2%; Score 2; DB 5; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 AK 2
 ||
 Db 10 AK 11

RESULT 32

Q99292
 ID Q99292 PRELIMINARY; PRT; 11 AA.
 AC Q99292;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Bicoid protein (Fragment).
 GN BCD.
 OS Drosophila heteroneura (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=32382;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91184004; PubMed=2081457;
 RA MacDonald P.M.;
 RT "bicoid mRNA localization signal: phylogenetic conservation of
 RT function and RNA secondary structure.";
 RL Development 110:161-171(1990).
 CC -!- FUNCTION: BICOID IS SEGMENT-POLARITY PROTEIN THAT PROVIDES
 CC POSITIONAL CUES FOR THE DEVELOPMENT OF HEAD AND THORACIC SEGMENTS.
 CC BCD REGULATES THE EXPRESSION OF ZYGOTIC GENES, POSSIBLY THROUGH
 CC ITS HOMEODOMAIN, AND INHIBITS THE ACTIVITY OF OTHER MATERNAL GENE
 CC PRODUCTS. IT IS POSSIBLE THAT BCD ALSO BINDS RNA.
 DR EMBL; M32125; AAA28386.1; -.
 DR FlyBase; FBgn0012352; Dhet\bcd.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0003723; F:RNA binding; IEA.
 DR GO; GO:0007275; P:development; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR GO; GO:0007367; P:segment polarity determination; IEA.
 KW DNA-binding; Developmental protein; Homeobox; Nuclear protein;
 KW RNA-binding; Segmentation polarity protein; Transcription regulation.
 FT NON_TER 1 1
 SQ SEQUENCE 11 AA; 1221 MW; 8CE802305DD9D6C1 CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;

Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 TQ 11
||
Db 4 TQ 5

RESULT 33

Q8MM58

ID Q8MM58 PRELIMINARY; PRT; 11 AA.
AC Q8MM58;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Mannose phosphate isomerase (Fragment).
GN MPI.
OS Heliconius cydno chioneus.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Papilionoidea; Nymphalidae; Heliconiinae; Heliconius.
OX NCBI_TaxID=171915;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=STRI-B-553-Mpi-1, and STRI-B-553-Mpi-2;
RA Bull V., Beltran M., Bermingham E., Jiggins C., McMillan O.,
RA Mallet J.;
RT "Molecular evidence for gene flow between species of Heliconius."
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF516222; AAM61908.1; -.
DR EMBL; AF516223; AAM61909.1; -.
DR GO; GO:0016853; F:isomerase activity; IEA.
KW Isomerase.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1312 MW; 56A67DB31DD1EAA3 CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KD 9
||
Db 4 KD 5

RESULT 34

Q86D32

ID Q86D32 PRELIMINARY; PRT; 11 AA.
AC Q86D32;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Histone H1 (Fragment).
OS Trypanosoma cruzi.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5693;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Dm28c;
 RX MEDLINE=22557728; PubMed=12670512;
 RA Sturm N.R., Vargas N.S., Westenberger S.J., Zingales B.,
 RA Campbell D.A.;
 RT "Evidence for multiple hybrid groups in Trypanosoma cruzi."
 RL Int. J. Parasitol. 33:269-279(2003).
 DR EMBL; AF545075; AAP21903.1; -.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1114 MW; CCC1B31E7772CDDD CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KK 3
 ||
 Db 9 KK 10

RESULT 35

Q86D31

ID Q86D31 PRELIMINARY; PRT; 11 AA.
 AC Q86D31;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Histone H1 (Fragment).
 OS Trypanosoma cruzi.
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
 OX NCBI_TaxID=5693;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sylvio X10;
 RX MEDLINE=22557728; PubMed=12670512;
 RA Sturm N.R., Vargas N.S., Westenberger S.J., Zingales B.,
 RA Campbell D.A.;
 RT "Evidence for multiple hybrid groups in Trypanosoma cruzi."
 RL Int. J. Parasitol. 33:269-279(2003).
 DR EMBL; AF545076; AAP21906.1; -.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1174 MW; CCD1B21E7772CDDD CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KK 3
 ||
 Db 9 KK 10

RESULT 36

Q95PX6

ID Q95PX6 PRELIMINARY; PRT; 11 AA.
 AC Q95PX6;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 GN ZK1236.8.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA None;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Favello A.;
 RT "The sequence of C. elegans cosmid ZK1236.";
 RL Submitted (MAY-1993) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Waterston R.;
 RT "Direct Submission.";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; L13200; AAL11108.1; -.
 DR WormPep; ZK1236.8; CE29629.
 KW Hypothetical protein.
 SQ SEQUENCE 11 AA; 1304 MW; DFA3510A25A76322 CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KK 3
 ||
 Db 8 KK 9

RESULT 37

Q9UEX7

ID Q9UEX7 PRELIMINARY; PRT; 11 AA.

AC Q9UEX7;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)

DE Human leucocyte antigen B (Fragment).

GN HLA-A*03.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.
 RA Fae I., Kriks D., Cernava B., Fischer G.F.;
 RT "An novel HLA-A*03 allele.";
 RL Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AJ252283; CAB65736.1; -.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1118 MW; 5191BC69C1A72DD7 CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 TQ 11
 ||
 Db 7 TQ 8

RESULT 38

077911
 ID 077911 PRELIMINARY; PRT; 11 AA.
 AC 077911;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE MHC class II B locus 3 (Fragment).
 OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidae;
 OC Cichlidae; Oreochromis.
 OX NCBI_TaxID=8128;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98315113; PubMed=9649539;
 RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
 RA Figueroa F., Sultmann H., Klein J.;
 RT "Linkage relationships and haplotype polymorphism among cichlid mhc
 RT class II B loci.";
 RL Genetics 149:1527-1537(1998).
 DR EMBL; AF050022; AAC41361.1; -.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1401 MW; 74342D9002D41B5B CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ER 5
 ||
 Db 8 ER 9

RESULT 39

Q8MEL7
 ID Q8MEL7 PRELIMINARY; PRT; 11 AA.

AC Q8MEL7;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Ribosomal protein 16 (Fragment).
 GN RPL16.
 OS Sida hookeriana.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Malvales; Malvaceae; Malvoideae; Sida.
 OX NCBI_TaxID=108446;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
 RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
 RT chloroplast DNA sequences of ndhF and the rpl16 intron."
 RL Syst. Bot. 27:333-350(2002).
 DR EMBL; AF384624; AAM50396.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RK 8
 ||
 Db 6 RK 7

RESULT 40

Q8MAZ1

ID Q8MAZ1 PRELIMINARY; PRT; 11 AA.
 AC Q8MAZ1;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE PsbJ (Fragment).
 GN PSBJ.
 OS Maripa paniculata.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC lamiids; Solanales; Convolvulaceae; Maripa.
 OX NCBI_TaxID=197411;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Stefanovic S., Krueger L., Olmstead R.G.;
 RT "Monophyly of the Convolvulaceae and circumscription of their major
 RT lineages based on DNA sequences of multiple chloroplast loci."
 RL Am. J. Bot. 0:0-0(2002).
 DR EMBL; AY100937; AAM55869.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.

KW Chloroplast.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1260 MW; 93736D59440861B1 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 DT 10
||
Db 3 DT 4

RESULT 41

Q8MB39

ID Q8MB39 PRELIMINARY; PRT; 11 AA.
AC Q8MB39;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE PsbJ (Fragment).
GN PSBJ.
OS *Wilsonia humilis*.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamiids; Solanales; Convolvulaceae; *Wilsonia*.
OX NCBI_TaxID=197481;
RN [1]
RP SEQUENCE FROM N.A.
RA Stefanovic S., Krueger L., Olmstead R.G.;
RT "Monophyly of the Convolvulaceae and circumscription of their major
RT lineages based on DNA sequences of multiple chloroplast loci.";
RL Am. J. Bot. 0:0-0(2002).
DR EMBL; AY100914; AAM55777.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1260 MW; 93736D59440861B1 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 DT 10
||
Db 3 DT 4

RESULT 42

Q8MEM2

ID Q8MEM2 PRELIMINARY; PRT; 11 AA.
AC Q8MEM2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein 16 (Fragment).

GN RPL16.
 OS Lagunaria patersonia.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Malvales; Malvaceae; Malvoideae; Lagunaria.
 OX NCBI_TaxID=183274;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
 RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
 RT chloroplast DNA sequences of ndhF and the rpl16 intron."
 RL Syst. Bot. 27:333-350(2002).
 DR EMBL; AF384616; AAM50388.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RK 8
 ||
 Db 6 RK 7

RESULT 43
 Q8MB58

ID Q8MB58 PRELIMINARY; PRT; 11 AA.
 AC Q8MB58;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE PsbJ (Fragment).
 GN PSBJ.
 OS Seddera hirsuta.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC lamiids; Solanales; Convolvulaceae; Seddera.
 OX NCBI_TaxID=197444;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Stefanovic S., Krueger L., Olmstead R.G.;
 RT "Monophyly of the Convolvulaceae and circumscription of their major
 RT lineages based on DNA sequences of multiple chloroplast loci."
 RL Am. J. Bot. 0:0-0(2002).
 DR EMBL; AY100905; AAM55743.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1260 MW; 93736D59440861B1 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;

Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 DT 10
||
Db 3 DT 4

RESULT 44

Q8MAZ3

ID Q8MAZ3 PRELIMINARY; PRT; 11 AA.
AC Q8MAZ3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE PsbJ (Fragment).
GN PSBJ.
OS Maripa repens.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamiids; Solanales; Convolvulaceae; Maripa.
OX NCBI_TaxID=197412;
RN [1]
RP SEQUENCE FROM N.A.
RA Stefanovic S., Krueger L., Olmstead R.G.;
RT "Monophyly of the Convolvulaceae and circumscription of their major
RT lineages based on DNA sequences of multiple chloroplast loci.";
RL Am. J. Bot. 0:0-0(2002).
DR EMBL; AY100936; AAM55865.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1260 MW; 93736D59440861B1 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 DT 10
||
Db 3 DT 4

RESULT 45

Q8MES5

ID Q8MES5 PRELIMINARY; PRT; 11 AA.
AC Q8MES5;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein 16 (Fragment).
GN RPL16.
OS Abelmoschus manihot.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC eurosids II; Malvales; Malvaceae; Malvoideae; Abelmoschus.
 OX NCBI_TaxID=183220;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
 RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
 RT chloroplast DNA sequences of ndhF and the rpl16 intron."
 RL Syst. Bot. 27:333-350(2002).
 DR EMBL; AF384561; AAM50399.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RK 8
 ||
 Db 6 RK 7

RESULT 46

Q8MEP0

ID Q8MEP0 PRELIMINARY; PRT; 11 AA.
 AC Q8MEP0;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Ribosomal protein 16 (Fragment).
 GN RPL16.
 OS Hibiscus peralbus.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Malvales; Malvaceae; Malvoideae; Hibiscus.
 OX NCBI_TaxID=183256;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
 RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
 RT chloroplast DNA sequences of ndhF and the rpl16 intron."
 RL Syst. Bot. 27:333-350(2002).
 DR EMBL; AF384598; AAM50370.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RK 8

Db ||
 6 RK 7

RESULT 47

Q8MES1

ID Q8MES1 PRELIMINARY; PRT; 11 AA.
AC Q8MES1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein 16 (Fragment).
GN RPL16.
OS Alyogyne pinoniana.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Malvales; Malvaceae; Malvoideae; Alyogyne.
OX NCBI_TaxID=183226;
RN [1]
RP SEQUENCE FROM N.A.
RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
RT chloroplast DNA sequences of ndhF and the rpl16 intron.";
RL Syst. Bot. 27:333-350(2002).
DR EMBL; AF384566; AAM50404.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RK 8
 ||
Db 6 RK 7

RESULT 48

Q8MEP3

ID Q8MEP3 PRELIMINARY; PRT; 11 AA.
AC Q8MEP3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein 16 (Fragment).
GN RPL16.
OS Hibiscus normanii.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Malvales; Malvaceae; Malvoideae; Hibiscus.
OX NCBI_TaxID=183253;
RN [1]

RP SEQUENCE FROM N.A.
 RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
 RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
 RT chloroplast DNA sequences of ndhF and the rpl16 intron.";
 RL Syst. Bot. 27:333-350(2002).
 DR EMBL; AF384595; AAM50367.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RK 8
 ||
 Db 6 RK 7

RESULT 49

Q8MBE1

ID Q8MBE1 PRELIMINARY; PRT; 11 AA.
 AC Q8MBE1;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE PsbJ (Fragment).
 GN PSBJ.
 OS Ipomoea alba.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC lamiids; Solanales; Convolvulaceae; Ipomoea.
 OX NCBI_TaxID=89634;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Stefanovic S., Krueger L., Olmstead R.G.;
 RT "Monophyly of the Convolvulaceae and circumscription of their major
 RT lineages based on DNA sequences of multiple chloroplast loci.";
 RL Am. J. Bot. 0:0-0(2002).
 DR EMBL; AY100861; AAM55568.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1260 MW; 93736D59440861B1 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 DT 10
 ||
 Db 3 DT 4

RESULT 50

Q8MEQ7

ID Q8MEQ7 PRELIMINARY; PRT; 11 AA.
 AC Q8MEQ7;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Ribosomal protein 16 (Fragment).
 GN RPL16.
 OS Hibiscus drummondii.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Malvales; Malvaceae; Malvoideae; Hibiscus.
 OX NCBI_TaxID=183239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
 RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
 RT chloroplast DNA sequences of ndhF and the rpl16 intron.";
 RL Syst. Bot. 27:333-350(2002).
 DR EMBL; AF384581; AAM50353.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RK 8
 ||
 Db 6 RK 7

RESULT 51

Q35374

ID Q35374 PRELIMINARY; PRT; 11 AA.
 AC Q35374;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE P1 protein (Fragment).
 OS Paramecium tetraurelia.
 OG Mitochondrion.
 OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;
 OC Paramecium.
 OX NCBI_TaxID=5888;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=stock 172;
 RX MEDLINE=87055241; PubMed=3023187;
 RA Pritchard A.E., Seilhamer J.J., Cummings D.J.;
 RT "Paramecium mitochondrial DNA sequences and RNA transcripts for
 RT cytochrome oxidase subunit I, URF1, and three ORFs adjacent to the

RT replication origin.";
 RL Gene 44:243-253(1986).
 DR EMBL; M15280; AAA79267.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1266 MW; 1D84259D16D046D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QR 7
 ||
 Db 7 QR 8

RESULT 52

Q8MEL9

ID Q8MEL9 PRELIMINARY; PRT; 11 AA.
 AC Q8MEL9;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Ribosomal protein 16 (Fragment).
 GN RPL16.
 OS Pavonia hastata.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Malvales; Malvaceae; Malvoideae; Pavonia.
 OX NCBI_TaxID=183278;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
 RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
 RT chloroplast DNA sequences of ndhF and the rpl16 intron."
 RL Syst. Bot. 27:333-350(2002).
 DR EMBL; AF384622; AAM50394.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RK 8
 ||
 Db 6 RK 7

RESULT 53

Q8MB77

ID Q8MB77 PRELIMINARY; PRT; 11 AA.

AC Q8MB77;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE PsbJ (Fragment).
 GN PSBJ.
 OS Odonellia hirtiflora.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC lamids; Solanales; Convolvulaceae; Odonellia.
 OX NCBI_TaxID=197424;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Stefanovic S., Krueger L., Olmstead R.G.;
 RT "Monophyly of the Convolvulaceae and circumscription of their major
 RT lineages based on DNA sequences of multiple chloroplast loci.";
 RL Am. J. Bot. 0:0-0(2002).
 DR EMBL; AY100897; AAM55711.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON TER 11 11
 SQ SEQUENCE 11 AA; 1260 MW; 93736D59440861B1 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 DT 10
 ||
 Db 3 DT 4

RESULT 54

Q8MERO

ID Q8MERO PRELIMINARY; PRT; 11 AA.
 AC Q8MERO;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Ribosomal protein 16 (Fragment).
 GN RPL16.
 OS Hibiscus coatesii.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Malvales; Malvaceae; Malvoideae; Hibiscus.
 OX NCBI_TaxID=183236;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
 RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
 RT chloroplast DNA sequences of ndhF and the rpl16 intron.";
 RL Syst. Bot. 27:333-350(2002).
 DR EMBL; AF384578; AAM50416.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.

FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RK 8
||
Db 6 RK 7

RESULT 55

Q8MES3

ID Q8MES3 PRELIMINARY; PRT; 11 AA.
AC Q8MES3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein 16 (Fragment).
GN RPL16.
OS Alyogyne cravenii.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Malvales; Malvaceae; Malvoideae; Alyogyne.
OX NCBI_TaxID=183223;
RN [1]
RP SEQUENCE FROM N.A.
RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
RT chloroplast DNA sequences of ndhF and the rpl16 intron.";
RL Syst. Bot. 27:333-350(2002).
DR EMBL; AF384563; AAM50401.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RK 8
||
Db 6 RK 7

RESULT 56

Q8MB79

ID Q8MB79 PRELIMINARY; PRT; 11 AA.
AC Q8MB79;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE PsbJ (Fragment).
 GN PSBJ.
 OS Aniseia argentina.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC lamiids; Solanales; Convolvulaceae; Aniseia.
 OX NCBI_TaxID=197349;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Stefanovic S., Krueger L., Olmstead R.G.;
 RT "Monophyly of the Convolvulaceae and circumscription of their major
 RT lineages based on DNA sequences of multiple chloroplast loci.";
 RL Am. J. Bot. 0:0-0(2002).
 DR EMBL; AY100895; AAM55703.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1260 MW; 93736D59440861B1 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 DT 10
 ||
 Db 3 DT 4

RESULT 57
 Q8MB97

ID Q8MB97 PRELIMINARY; PRT; 11 AA.
 AC Q8MB97;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE PsbJ (Fragment).
 GN PSBJ.
 OS Merremia peltata.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC lamiids; Solanales; Convolvulaceae; Merremia.
 OX NCBI_TaxID=197416;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Stefanovic S., Krueger L., Olmstead R.G.;
 RT "Monophyly of the Convolvulaceae and circumscription of their major
 RT lineages based on DNA sequences of multiple chloroplast loci.";
 RL Am. J. Bot. 0:0-0(2002).
 DR EMBL; AY100885; AAM55663.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1260 MW; 93736D59440861B1 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;

Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 DT 10
||
Db 3 DT 4

RESULT 58

Q8MEP5

ID Q8MEP5 PRELIMINARY; PRT; 11 AA.
AC Q8MEP5;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein 16 (Fragment).
GN RPL16.
OS Hibiscus microchlaenus.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Malvales; Malvaceae; Malvoideae; Hibiscus.
OX NCBI_TaxID=183251;
RN [1]
RP SEQUENCE FROM N.A.
RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
RT chloroplast DNA sequences of ndhF and the rpl16 intron."
RL Syst. Bot. 27:333-350(2002).
DR EMBL; AF384593; AAM50365.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RK 8
||
Db 6 RK 7

RESULT 59

Q8MER1

ID Q8MER1 PRELIMINARY; PRT; 11 AA.
AC Q8MER1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein 16 (Fragment).
GN RPL16.
OS Hibiscus calyphyllus.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Malvales; Malvaceae; Malvoideae; Hibiscus.
 OX NCBI_TaxID=183235;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
 RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
 RT chloroplast DNA sequences of ndhF and the rpl16 intron."
 RL Syst. Bot. 27:333-350(2002).
 DR EMBL; AF384577; AAM50415.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RK 8
 ||
 Db 6 RK 7

RESULT 60

Q8MER7

ID Q8MER7 PRELIMINARY; PRT; 11 AA.
 AC Q8MER7;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Ribosomal protein 16 (Fragment).
 GN RPL16.
 OS Fioria vitifolia.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Malvales; Malvaceae; Malvoideae; Fioria.
 OX NCBI_TaxID=183231;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
 RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
 RT chloroplast DNA sequences of ndhF and the rpl16 intron."
 RL Syst. Bot. 27:333-350(2002).
 DR EMBL; AF384570; AAM50408.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RK 8
||
Db 6 RK 7

RESULT 61

Q38415
ID Q38415 PRELIMINARY; PRT; 11 AA.
AC Q38415;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ant1 protein (Fragment).
OS Bacteriophage P7.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
OC P1-like viruses.
OX NCBI_TaxID=10682;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90335968; PubMed=1696181;
RA Citron M., Schuster H.;
RT "The c4 repressors of bacteriophages P1 and P7 are antisense RNAs.";
RL Cell 62:591-598(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92319637; PubMed=1620606;
RA Citron M., Schuster H.;
RT "The c4 repressor of bacteriophage P1 is a processed 77 base antisense
RT RNA.";
RL Nucleic Acids Res. 20:3085-3090(1992).
DR EMBL; M35139; AAA32437.1; -.
DR PIR; S42449; S42449.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1315 MW; 38A55C6D11B2C737 CRC64;

Query Match 18.2%; Score 2; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KK 3
||
Db 2 KK 3

RESULT 62

Q37925
ID Q37925 PRELIMINARY; PRT; 11 AA.
AC Q37925;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Bacteriophage fr replicase (Fragment).
OS Bacteriophage fr.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Levivirus.
OX NCBI_TaxID=12017;
RN [1]

RP SEQUENCE FROM N.A.
RA Berzin V.M., Gribov V.A., Cielens I.E., Jansone I.V., Gren E.J.;
RT "The nucleotide sequence of the regulatory region of phage fr
RT replicase cistron.";
RL Bioorg. Khim. 7:306-308(1981).
DR EMBL; M34834; AAA32193.1; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1285 MW; 8BD43470C33321B1 CRC64;

Query Match 18.2%; Score 2; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KK 3
||
Db 6 KK 7

RESULT 63
Q9S8X4
ID Q9S8X4 PRELIMINARY; PRT; 11 AA.
AC Q9S8X4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Vegetative storage protein 94 peptide 3, VSP94=LIPOXYGENASE
DE (Fragment).
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE.
RX MEDLINE=92361246; PubMed=1822994;
RA Tranbarger T.J., Franceschi V.R., Hildebrand D.F., Grimes H.D.;
RT "The soybean 94-kilodalton vegetative storage protein is a
RT lipoxygenase that is localized in paraveinal mesophyll cell
RT vacuoles.";
RL Plant Cell 3:973-987(1991).
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1366 MW; 9B337C3C0DD9CB1A CRC64;

Query Match 18.2%; Score 2; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ER 5
||
Db 9 ER 10

RESULT 64
Q39784
ID Q39784 PRELIMINARY; PRT; 11 AA.
AC Q39784;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last annotation update)
 DE Alcohol dehydrogenase 2b-2 (Fragment).
 OS Gossypium hirsutum (Upland cotton).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
 OX NCBI_TaxID=3635;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Blue Tag Siokra;
 RA Millar A.A., Dennis E.S.;
 RL Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; U53705; AAA98988.1; -.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1161 MW; D67F443942D6D87D CRC64;

Query Match 18.2%; Score 2; DB 10; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2
 ||
 Db 10 AK 11

RESULT 65
 O82070

ID O82070 PRELIMINARY; PRT; 11 AA.
 AC O82070;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE RNA polymerase (EC 2.7.7.6) (Fragment).
 OS Triticum aestivum (Wheat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
 OC Triticeae; Triticum.
 OX NCBI_TaxID=4565;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Chinese Spring;
 RA Young D.A., Allen R., Harvey A.J., Lonsdale D.M.;
 RT "Characterization of a gene encoding a single-subunit RNA polymerase
 RT from maize which is alternatively spliced."
 RL Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AJ005344; CAA06489.1; -.
 DR GO; GO:0003899; F:DNA-directed RNA polymerase activity; IEA.
 DR GO; GO:0003900; F:DNA-directed RNA polymerase I activity; IEA.
 DR GO; GO:0003901; F:DNA-directed RNA polymerase II activity; IEA.
 DR GO; GO:0003902; F:DNA-directed RNA polymerase III activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 KW Nucleotidyltransferase; Transferase.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1329 MW; CD96344923240AB2 CRC64;

Query Match 18.2%; Score 2; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RK 8
||
Db 6 RK 7

RESULT 66

Q04131

ID Q04131 PRELIMINARY; PRT; 11 AA.
AC Q04131;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Wound induced protein (Fragment).
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamiids; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=pik-red; TISSUE=Pericarp;
RX MEDLINE=91355936; PubMed=1715787;
RA Parsons B.L., Mattoo A.K.;
RT "Wound regulated accumulation of specific transcripts in tomato fruit:
RT interactions with fruit development, ethylene and light."
RL Plant Mol. Biol. 17:453-464(1991).
DR EMBL; X59884; CAA42539.1; -.
DR PIR; S19775; S19775.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1278 MW; 92CB257828733325 CRC64;

Query Match 18.2%; Score 2; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KK 3
||
Db 5 KK 6

RESULT 67

P83092

ID P83092 PRELIMINARY; PRT; 11 AA.
AC P83092;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 33.6 kDa protein (Fragment).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Amaranthaceae; Spinacia.

OX NCBI_TaxID=3562;
 RN [1]
 RP SEQUENCE, AND SUBCELLULAR LOCATION.
 RA Schubert M., Peterson U., Funk C., Schroeder W.P., Kieselbach T.;
 RL Submitted (AUG-2001) to Swiss-Prot.
 CC -!- SUBCELLULAR LOCATION: CHLOROPLAST; WITHIN THE THYLAKOID LUMEN.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1274 MW; 95344C4D21AAB775 CRC64;

Query Match 18.2%; Score 2; DB 10; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 DT 10
 ||
 Db 6 DT 7

RESULT 68

P97755
 ID P97755 PRELIMINARY; PRT; 11 AA.
 AC P97755;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
 DE Secretogranin II (SGII) (Fragment).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96343805; PubMed=8756552;
 RA Jones L.C., Day R.N., Pittler S.J., Valentine D.L., Scammell J.G.;
 RT "Cell-specific expression of the rat secretogranin II promoter."
 RL Endocrinology 137:3815-3822(1996).
 DR EMBL; AF107301; -; NOT_ANNOTATED_CDS.
 FT NON_TER 1 1
 SQ SEQUENCE 11 AA; 1298 MW; 3E4E8DA446C1B5A7 CRC64;

Query Match 18.2%; Score 2; DB 11; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 TQ 11
 ||
 Db 6 TQ 7

RESULT 69

Q99N81
 ID Q99N81 PRELIMINARY; PRT; 11 AA.
 AC Q99N81;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE Delta like 1 (Fragment).
 GN DLL1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Nakayama K.;
 RT "Multiple POU-binding motifs, recognized by tissue-specific nuclear
 RT factor(S), are important for Dll1 gene expression in developing neural
 RT precursor cells."
 RL Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AB050457; BAB43867.1; -.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1259 MW; 33C3634CBDC40B07 CRC64;

Query Match 18.2%; Score 2; DB 11; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ER 5
 ||
 Db 5 ER 6

RESULT 70

Q9JLE6

ID Q9JLE6 PRELIMINARY; PRT; 11 AA.
 AC Q9JLE6;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE Thioredoxin reductase (Fragment).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Rundlof A.-K., Arner E.S.J.;
 RT "Genomic sequence of parts of the rat thioredoxin reductase 1 gene."
 RL Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF189711; AAF26304.1; -.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1255 MW; 804D1A1E6DDAA325 CRC64;

Query Match 18.2%; Score 2; DB 11; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KD 9
 ||
 Db 5 KD 6

RESULT 71

Q8R2J7

ID Q8R2J7 PRELIMINARY; PRT; 11 AA.
 AC Q8R2J7;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Microphthalmia-associated transcription factor (Fragment).
 GN MITF.
 OS Mesocricetus auratus (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Mesocricetus.
 OX NCBI_TaxID=10036;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RA Graw J., Pretsch W., Loester I.;
 RT "Mutation in intron 6 of the hamster mitf gene leads to skipping of
 RT the subsequent exon and creates a dominant animal model for the human
 RT Waardenburg syndrome type II."
 RL Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AJ458439; CAD30263.1; -.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1532 MW; 69D76B515449D414 CRC64;

Query Match 18.2%; Score 2; DB 11; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ER 5
 ||
 Db 1 ER 2

RESULT 72

P89269

ID P89269 PRELIMINARY; PRT; 11 AA.
 AC P89269;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE DNA binding protein homolog (Fragment).
 OS Xestia c-nigrum granulosis virus (XnGV) (Xestia c-nigrum
 OS granulovirus).
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae; Granulovirus.
 OX NCBI_TaxID=51677;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=alpha-4;
 RX MEDLINE=98271593; PubMed=9608666;
 RA Goto C., Hayakawa T., Maeda S.;
 RT "Genome organization of Xestia c-nigrum granulovirus."
 RL Virus Genes 16:199-210(1998).
 DR EMBL; U70897; AAB46487.1; -.
 FT NON_TER 1 1

SQ SEQUENCE 11 AA; 1371 MW; 6F05444F52C1E454 CRC64;

Query Match 18.2%; Score 2; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QR 7
||
Db 2 QR 3

RESULT 73

Q84073

ID Q84073 PRELIMINARY; PRT; 11 AA.
AC Q84073;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Influenza A/fpv/rostock/34 (H7n1), polymerase 3 (Seg 3), 3' end of
DE vrna (Initiator region for protein coding) (Fragment).
OS Influenzavirus A.
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses.
OX NCBI_TaxID=197911;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=80034428; PubMed=493121;
RA Robertson J.S.;
RT "5' and 3' terminal nucleotide sequences of the rna genome segments of
RT influenza virus."
RL Nucleic Acids Res. 6:3745-3757(1979).
DR EMBL; J02123; AAA43612.1; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1400 MW; CC2007F7A6C412C9 CRC64;

Query Match 18.2%; Score 2; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQ 6
||
Db 6 RQ 7

RESULT 74

Q69269

ID Q69269 PRELIMINARY; PRT; 11 AA.
AC Q69269;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
GN IE.
OS Equine herpesvirus 1.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
OX NCBI_TaxID=10326;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Kentucky A;
 RX MEDLINE=90064773; PubMed=2555546;
 RA Harty R.N., Colle C.F., Grundy F.J., O'Callaghan D.J.;
 RT "Mapping the termini and intron of the spliced immediate-early
 transcript of equine herpesvirus 1."
 RL J. Virol. 63:5101-5110(1989).
 DR EMBL; M30497; AAA66553.1; -.
 KW Hypothetical protein.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1224 MW; D93837E0CAB5A416 CRC64;

Query Match 18.2%; Score 2; DB 12; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QR 7
 ||
 Db 4 QR 5

RESULT 75

Q800X7

ID Q800X7 PRELIMINARY; PRT; 11 AA.
 AC Q800X7;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Vacuolar H-ATPase B subunit (Fragment).
 OS Chelydra serpentina serpentina (common snapping turtle).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Testudines; Cryptodira; Testudinoidea; Chelydridae; Chelydra.
 OX NCBI_TaxID=134619;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21876906; PubMed=11882478;
 RA Trudeau V.L., Chiu S., Kennedy S.W., Brooks R.J.;
 RT "Octylphenol (OP) alters the expression of members of the amyloid
 protein family in the hypothalamus of the snapping turtle, Chelydra
 serpentina serpentina."
 RL Environ. Health Perspect. 110:269-275(2002).
 DR EMBL; AF469184; AAO48730.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 11 AA; 1350 MW; 2FC8B6D0B5BAB417 CRC64;

Query Match 18.2%; Score 2; DB 13; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2
 ||
 Db 9 AK 10

Search completed: April 8, 2004, 15:46:01
 Job time : 28.7692 secs

OM protein - protein search, using sw model

Run on: April 8, 2004, 15:30:07 ; Search time 5.15385 Seconds
 (without alignments)
 111.135 Million cell updates/sec

Title: US-09-787-443A-2
 Perfect score: 11
 Sequence: 1 AKKERQRKDTQ 11

Scoring table: OLIGO
 Gapop 60.0 , Gapext 60.0

Searched: 141681 seqs, 52070155 residues

Word size : 0

Total number of hits satisfying chosen parameters: 70

Minimum DB seq length: 11

Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		Length	DB	ID	Description
		Match					
1	2	18.2		11	1	ASL2_BACSE	P83147 bacteroides
2	2	18.2		11	1	BRK_MEGFL	P12797 megascolia
3	2	18.2		11	1	NXSN_PSETE	P59072 pseudonaja
4	2	18.2		11	1	PKC1_CARMO	P82684 carausius m
5	2	18.2		11	1	PQQC_PSEFL	P55173 pseudomonas
6	2	18.2		11	1	Q2OA_COMTE	P80464 comamonas t
7	2	18.2		11	1	TKNA_RANRI	P29207 rana ridibu
8	2	18.2		11	1	TKND_RANCA	P22691 rana catesb
9	2	18.2		11	1	TKN_ELEMO	P01293 eledone mos
10	2	18.2		11	1	UXB2_YEAST	P99013 saccharomyc
11	1	9.1		11	1	ANGT_CRIGE	P09037 crinia geor
12	1	9.1		11	1	ASL1_BACSE	P83146 bacteroides
13	1	9.1		11	1	BPP3_BOTIN	P30423 bothrops in
14	1	9.1		11	1	BPP4_BOTIN	P30424 bothrops in
15	1	9.1		11	1	BPPB_AGKHA	P01021 agkistrodon
16	1	9.1		11	1	BPP_AGKHP	P04562 agkistrodon
17	1	9.1		11	1	CA21_LITCI	P82087 litoria cit

18	1	9.1	11	1	CA22_LITCI	P82088	litoria cit
19	1	9.1	11	1	CA31_LITCI	P82089	litoria cit
20	1	9.1	11	1	CA32_LITCI	P82090	litoria cit
21	1	9.1	11	1	CA41_LITCI	P82091	litoria cit
22	1	9.1	11	1	CA42_LITCI	P82092	litoria cit
23	1	9.1	11	1	CEP1_ACHFU	P22790	achatina fu
24	1	9.1	11	1	CORZ_PERAM	P11496	periplaneta
25	1	9.1	11	1	COXA_CANFA	P99501	canis famil
26	1	9.1	11	1	CSI5_BACSU	P81095	bacillus su
27	1	9.1	11	1	CX5A_CONAL	P58848	conus aulic
28	1	9.1	11	1	CX5B_CONAL	P58849	conus aulic
29	1	9.1	11	1	CXL1_CONMR	P58807	conus marmo
30	1	9.1	11	1	EFG_CLOPA	P81350	clostridium
31	1	9.1	11	1	ES1_RAT	P56571	rattus norv
32	1	9.1	11	1	FAR6_PENMO	P83321	penaeus mon
33	1	9.1	11	1	FAR9_CALVO	P41864	calliphora
34	1	9.1	11	1	HS70_PINPS	P81672	pinus pinas
35	1	9.1	11	1	LADD_ONCMY	P81018	oncorhynch
36	1	9.1	11	1	LPW_THETH	P05624	thermus the
37	1	9.1	11	1	LSK1_LEUMA	P04428	leucophaea
38	1	9.1	11	1	LSKP_PERAM	P36885	periplaneta
39	1	9.1	11	1	MHBI_KLEPN	P80580	klebsiella
40	1	9.1	11	1	MLG_THETS	P41989	theromyzon
41	1	9.1	11	1	MORN_HUMAN	P01163	homo sapien
42	1	9.1	11	1	NUHM_CANFA	P49820	canis famil
43	1	9.1	11	1	OAIF_SARBU	P83518	sarcophaga
44	1	9.1	11	1	PVK1_PERAM	P41837	periplaneta
45	1	9.1	11	1	RANC_RANPI	P08951	rana pipien
46	1	9.1	11	1	RE41_LITRU	P82074	litoria rub
47	1	9.1	11	1	RR2_CONAM	P42341	conopholis
48	1	9.1	11	1	RRPL_CHAV	P13179	chandipura
49	1	9.1	11	1	RS30_ONCMY	P83328	oncorhynch
50	1	9.1	11	1	T2P1_PROVU	P31031	proteus vul
51	1	9.1	11	1	TIN1_HOPTI	P82651	hoplobatrac
52	1	9.1	11	1	TIN4_HOPTI	P82654	hoplobatrac
53	1	9.1	11	1	TKC2_CALVO	P41518	calliphora
54	1	9.1	11	1	TKN1_PSEGU	P42986	pseudophryn
55	1	9.1	11	1	TKN1_UPEIN	P82026	uperoleia i
56	1	9.1	11	1	TKN1_UPERU	P08612	uperoleia r
57	1	9.1	11	1	TKN2_PSEGU	P42987	pseudophryn
58	1	9.1	11	1	TKN2_UPERU	P08616	uperoleia r
59	1	9.1	11	1	TKN3_PSEGU	P42988	pseudophryn
60	1	9.1	11	1	TKN4_PSEGU	P42989	pseudophryn
61	1	9.1	11	1	TKN5_PSEGU	P42990	pseudophryn
62	1	9.1	11	1	TKNA_CHICK	P19850	gallus gall
63	1	9.1	11	1	TKNA_GADMO	P28498	gadus morhu
64	1	9.1	11	1	TKNA_HORSE	P01290	equus cabal
65	1	9.1	11	1	TKNA_ONCMY	P28499	oncorhynch
66	1	9.1	11	1	TKNA_RANCA	P22688	rana catesb
67	1	9.1	11	1	TKNA_SCYCA	P41333	scyliorhinu
68	1	9.1	11	1	TKN_PHYFU	P08615	physalaemus
69	1	9.1	11	1	UF05_MOUSE	P38643	mus musculu
70	1	9.1	11	1	ULAG_HUMAN	P31933	homo sapien

ALIGNMENTS

RESULT 1

ASL2_BACSE

ID ASL2_BACSE STANDARD; PRT; 11 AA.
AC P83147;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Acharan sulfate lyase 2 (EC 4.2.2.-) (Fragment).
OS Bacteroides stercoris.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=46506;
RN [1]
RP SEQUENCE, FUNCTION, ENZYME REGULATION, AND SUBUNIT.
RC STRAIN=HJ-15;
RX MEDLINE=21223019; PubMed=11322884;
RA Kim B.-T., Hong S.-W., Kim W.-S., Kim Y.S., Kim D.-H.;
RT "Purification and characterization of acharan sulfate lyases, two
RT novel heparinases, from Bacteroides stercoris HJ-15."
RL Eur. J. Biochem. 268:2635-2641(2001).
CC -!- FUNCTION: Degrades acharan sulfate and, to a lesser extent,
CC heparin and heparan sulfate.
CC -!- ENZYME REGULATION: Inhibited by cupric ion, nitrogen and lead.
CC Activated by reducing agents, such as DL-dithiothreitol and 2-
CC mercaptoethanol.
CC -!- SUBUNIT: Monomer.
CC -!- PTM: The N-terminus is blocked.
CC -!- MISCELLANEOUS: Has an isoelectric point of 8.6. Its optimum pH is
CC 7.2 and optimum temperature 45 degrees Celsius.
KW Lyase; Heparin-binding.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1195 MW; D79D897C7AA451AD CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QR 7
||
Db 10 QR 11

RESULT 2

BRK_MEGFL

ID BRK_MEGFL STANDARD; PRT; 11 AA.
AC P12797;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Megascoliakinin ([Thr6]bradykinin-Lys-Ala) [Contains: Bradykinin-like
DE peptide ([Thr6]bradykinin)].
OS Megascolia flavifrons (Garden dagger wasp) (Solitary wasp).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Scoliidae; Megascolia.

OX NCBI_TaxID=7437;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=87293024; PubMed=3617088;
 RA Yasuhara T., Mantel P., Nakajima T., Piek T.;
 RT "Two kinins isolated from an extract of the venom reservoirs of the
 RT solitary wasp *Megascolia flavifrons*.";
 RL Toxicon 25:527-535(1987).
 RN [2]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RA Nakajima T., Piek T., Yashuara T., Mantel P.;
 RT "Two kinins isolated from the venom of *Megascolia flavifrons*.";
 RL Toxicon 26:34-34(1988).
 CC -!- FUNCTION: Both proteins have bradykinin-like, although lower
 CC activities (e.g. smooth muscle contraction).
 CC -!- SUBCELLULAR LOCATION: Secreted; wasp venom reservoirs.
 CC -!- SIMILARITY: Belongs to the bradykinin family.
 DR PIR; B26744; B26744.
 DR GO; GO:0005615; C:extracellular space; IDA.
 DR GO; GO:0045776; P:negative regulation of blood pressure; ISS.
 DR GO; GO:0045987; P:positive regulation of smooth muscle contra. . .; TAS.
 KW Bradykinin; Vasodilator.
 FT PEPTIDE 1 11 MEGASCOLIAKININ.
 FT PEPTIDE 1 9 BRADYKININ-LIKE PEPTIDE.
 SQ SEQUENCE 11 AA; 1273 MW; 33867393D771A9C8 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RK 8
 ||
 Db 9 RK 10

RESULT 3

NXSN_PSETE
 ID NXSN_PSETE STANDARD; PRT; 11 AA.
 AC P59072;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Short neurotoxin N1 (Alpha neurotoxin) (Fragment).
 OS Pseudonaja textilis (Eastern brown snake).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Acanthophiinae; Pseudonaja.
 OX NCBI_TaxID=8673;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Venom;
 RX MEDLINE=99449602; PubMed=10518793;
 RA Gong N.L., Armugam A., Jeyaseelan K.;
 RT "Postsynaptic short-chain neurotoxins from *Pseudonaja textilis*: cDNA
 RT cloning, expression and protein characterization.";

RL Eur. J. Biochem. 265:982-989(1999).
 CC -!- FUNCTION: Lethal neurotoxin, binds and inhibits nicotinic
 CC acetylcholine receptors (nAChR).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
 CC -!- MASS SPECTROMETRY: MW=6236; METHOD=Electrospray.
 CC -!- MISCELLANEOUS: LD(50) is 0.84 mg/kg by intravenous injection.
 CC -!- SIMILARITY: Belongs to the snake toxin family.
 DR InterPro; IPR003571; Snake_toxin.
 DR PROSITE; PS00272; SNAKE_TOXIN; PARTIAL.
 KW Toxin; Neurotoxin; Postsynaptic neurotoxin;
 KW Acetylcholine receptor inhibitor; Multigene family.
 FT UNSURE 3 3
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1319 MW; 0D1EF0C81B58732B CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 DT 10
 ||
 Db 9 DT 10

RESULT 4

PKC1_CARMO

ID PKC1_CARMO STANDARD; PRT; 11 AA.
 AC P82684;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pyrokinin-1 (Cam-PK-1) (FXPRL-Amide).
 OS Carausius morosus (Indian stick insect).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Phasmatodea; Euphasmida; Phasmatoidea;
 OC Heteronemiidae; Carausius.
 OX NCBI_TaxID=7022;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC TISSUE=Corpora cardiaca;
 RA Predel R., Kellner R., Gaede G.;
 RT "Myotropic neuropeptides from the retrocerebral complex of the stick
 RT insect, Carausius morosus (Phasmatodea: Lonchodidae).";
 RL Eur. J. Entomol. 96:275-278(1999).
 CC -!- FUNCTION: Mediates visceral muscle contractile activity (myotropic
 CC activity).
 CC -!- MASS SPECTROMETRY: MW=1235; METHOD=MALDI.
 CC -!- SIMILARITY: Belongs to the pyrokinin family.
 DR InterPro; IPR001484; Pyrokinin.
 DR PROSITE; PS00539; PYROKININ; FALSE_NEG.
 KW Neuropeptide; Amidation; Pyrokinin.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1236 MW; 2BFA5225BB46C1A8 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 TQ 11
||
Db 5 TQ 6

RESULT 5

PQQC_PSEFL

ID PQQC_PSEFL STANDARD; PRT; 11 AA.

AC P55173;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Coenzyme PQQ synthesis protein C (Pyrroloquinoline quinone

DE biosynthesis protein C) (Fragment).

GN PQQC.

OS Pseudomonas fluorescens.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

OC Pseudomonadaceae; Pseudomonas.

OX NCBI_TaxID=294;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CHA0;

RX MEDLINE=96064397; PubMed=8526497;

RA Schnider U., Keel C., Defago G., Haas D.;

RT "Tn5-directed cloning of pqq genes from Pseudomonas fluorescens CHA0:

RT mutational inactivation of the genes results in overproduction of the

RT antibiotic pyoluteorin.";

RL Appl. Environ. Microbiol. 61:3856-3864(1995).

CC -!- PATHWAY: Pyrroloquinoline quinone (PQQ) biosynthesis.

CC -!- SIMILARITY: Belongs to the pqqC family.

CC

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CC

DR EMBL; X87299; CAA60734.1; -.

DR PIR; S58244; S58244.

DR HAMAP; MF_00654; -; 1.

KW PQQ biosynthesis.

FT NON_TER 11 11

SQ SEQUENCE 11 AA; 1182 MW; 89DF46E4C5B73771 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.2e+04;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 DT 10
||
Db 3 DT 4

RESULT 6

Q2OA_COMTE

ID Q2OA_COMTE STANDARD; PRT; 11 AA.
 AC P80464;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Quinoline 2-oxidoreductase, alpha chain (EC 1.3.99.17) (Fragment).
 OS Comamonas testosteroni (Pseudomonas testosteroni).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Comamonadaceae; Comamonas.
 OX NCBI_TaxID=285;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=63;
 RX MEDLINE=96035889; PubMed=7556204;
 RA Schach S., Tshisuaka B., Fetzner S., Lingens F.;
 RT "Quinoline 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline 5,6-
 RT dioxygenase from Comamonas testosteroni 63. The first two enzymes in
 RT quinoline and 3-methylquinoline degradation.";
 RL Eur. J. Biochem. 232:536-544(1995).
 CC -!- FUNCTION: Converts (3-methyl-)-quinoline to (3-methyl-)2-oxo-
 CC 1,2-dihydroquinoline.
 CC -!- CATALYTIC ACTIVITY: Quinoline + acceptor + H(2)O = isoquinolin-
 CC 1(2H)-one + reduced acceptor.
 CC -!- COFACTOR: FAD, molybdenum and iron-sulfur.
 CC -!- PATHWAY: Degradation of quinoline and (3-methyl-)quinoline; first
 CC step.
 CC -!- SUBUNIT: Heterohexamer of two alpha chains, two beta chains, and
 CC two gamma chains (Probable).
 DR PIR; S66606; S66606.
 KW Oxidoreductase; Flavoprotein; FAD; Molybdenum.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1213 MW; 869094322B1DC2CA CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2
 ||
 Db 1 AK 2

RESULT 7

TKNA_RANRI

ID TKNA_RANRI STANDARD; PRT; 11 AA.
 AC P29207;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ranakinin (Substance-P-related peptide).
 OS Rana ridibunda (Laughing frog) (Marsh frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
 OX NCBI_TaxID=8406;
 RN [1]

RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=92044543; PubMed=1658233;
 RA O'Harte F., Burcher E., Lovas S., Smith D.D., Vaudry H., Conlon J.M.;
 RT "Ranakinin: a novel NK1 tachykinin receptor agonist isolated with
 RT neurokinin B from the brain of the frog *Rana ridibunda*.";
 RL J. Neurochem. 57:2086-2091(1991).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR InterPro; IPR008215; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Tachykinin; Neuropeptide; Amidation.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1352 MW; 3A2460CC59D40B07 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ER 5
 ||
 Db 5 ER 6

RESULT 8

TKND_RANCA

ID TKND_RANCA STANDARD; PRT; 11 AA.
 AC P22691;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ranatachykinin D (RTK D).
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
 OX NCBI_TaxID=8400;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Intestine;
 RX MEDLINE=91254337; PubMed=2043143;
 RA Kozawa H., Hino J., Minamino N., Kangawa K., Matsuo H.;
 RT "Isolation of four novel tachykinins from frog (*Rana catesbeiana*)
 RT brain and intestine.";
 RL Biochem. Biophys. Res. Commun. 177:588-595(1991).
 RN [2]
 RP SEQUENCE.
 RC TISSUE=Intestine;
 RX MEDLINE=94023216; PubMed=8210506;
 RA Kangawa K., Kozawa H., Hino J., Minamino N., Matsuo H.;
 RT "Four novel tachykinins in frog (*Rana catesbeiana*) brain and

RT intestine.";
 RL Regul. Pept. 46:81-88(1993).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; D61033; D61033.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR PROSITE; PS00267; TACHYKININ; FALSE_NEG.
 KW Tachykinin; Neuropeptide; Amidation.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1350 MW; 3A34256C59D40B07 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ER 5
 ||
 Db 5 ER 6

RESULT 9

TKN_ELEMO

ID TKN_ELEMO STANDARD; PRT; 11 AA.
 AC P01293;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Eledoisin.
 OS Eledone moschata (Musky octopus) (Ozaena moschata), and
 OS Eledone cirrhosa (Curled octopus) (Ozaena cirrosa).
 OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
 OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Eledone.
 OX NCBI_TaxID=6641, 102876;
 RN [1]
 RP SEQUENCE.
 RA Anastasi A., Erspamer V.;
 RT "The isolation and amino acid sequence of eledoisin, the active
 RT endecapeptide of the posterior salivary glands of Eledone.";
 RL Arch. Biochem. Biophys. 101:56-65(1963).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; A01561; EOOC.
 DR PIR; B01561; EOCC.
 DR PDB; 1MXQ; 18-FEB-03.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Tachykinin; Neuropeptide; Amidation; Pyrrolidone carboxylic acid;
 KW 3D-structure.

FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1206 MW; 570D7C2559CDDAA3 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KD 9
 ||
 Db 4 KD 5

RESULT 10

UXB2_YEAST

ID UXB2_YEAST STANDARD; PRT; 11 AA.
 AC P99013;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Unknown protein from 2D-page (Spot 2D-000K2F) (Fragment).
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=X2180-1A;
 RA Sanchez J.-C., Golaz O., Schaller D., Morch F., Frutiger S.,
 RA Hughes G.J., Appel R.D., Deshusses J., Hochstrasser D.F.;
 RL Submitted (AUG-1995) to Swiss-Prot.
 CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
 CC protein is: 6.20, its MW is: 9.2 kDa.
 DR SWISS-2DPAGE; P99013; YEAST.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1328 MW; EC38021C0DCB42DA CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RK 8
 ||
 Db 8 RK 9

RESULT 11

ANGT_CRIGE

ID ANGT_CRIGE STANDARD; PRT; 11 AA.
 AC P09037;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Crinia-angiotensin II.
 OS Crinia georgiana (Quacking frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;

OC Myobatrachinae; Crinia.
 OX NCBI_TaxID=8374;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=80024575; PubMed=488254;
 RA Erspamer V., Melchiorri P., Nakajima T., Yasuhara T., Endean R.;
 RT "Amino acid composition and sequence of crinia-angiotensin, an
 RT angiotensin II-like endcapeptide from the skin of the Australian
 RT frog *Crinia georgiana*.";
 RL Experientia 35:1132-1133(1979).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 DR PIR; S07207; S07207.
 KW Vasoconstrictor.
 SQ SEQUENCE 11 AA; 1271 MW; 8A0921F7DB50440A CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.2e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
 |
 Db 1 A 1

RESULT 12

ASL1_BACSE

ID ASL1_BACSE STANDARD; PRT; 11 AA.
 AC P83146;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Acharan sulfate lyase 1 (EC 4.2.2.-) (Fragment).
 OS Bacteroides stercoris.
 OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
 OC Bacteroidaceae; Bacteroides.
 OX NCBI_TaxID=46506;
 RN [1]
 RP SEQUENCE, FUNCTION, ENZYME REGULATION, AND SUBUNIT.
 RC STRAIN=HJ-15;
 RX MEDLINE=21223019; PubMed=11322884;
 RA Kim B.-T., Hong S.-W., Kim W.-S., Kim Y.S., Kim D.-H.;
 RT "Purification and characterization of acharan sulfate lyases, two
 RT novel heparinases, from *Bacteroides stercoris* HJ-15.";
 RL Eur. J. Biochem. 268:2635-2641(2001).
 CC -!- FUNCTION: Degrades acharan sulfate and, to a lesser extent,
 CC heparin and heparan sulfate.
 CC -!- ENZYME REGULATION: Inhibited by cupric ion, nitrogen and cobalt.
 CC Activated by reducing agents, such as DL-dithiothreitol and 2-
 CC mercaptoethanol.
 CC -!- SUBUNIT: Monomer.
 CC -!- PTM: The N-terminus is blocked.
 CC -!- MISCELLANEOUS: Has an isoelectric point of 8.6. Its optimum pH is
 CC 7.2 and optimum temperature 45 degrees Celsius.
 KW Lyase; Heparin-binding.
 FT NON_TER 1 1

FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1395 MW; 01B2DAA241E865AB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.2e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6
|
Db 11 Q 11

RESULT 13

BPP3_BOTIN

ID BPP3_BOTIN STANDARD; PRT; 11 AA.
AC P30423;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S4,3,2 (10C) (Angiotensin-converting
DE enzyme inhibitor).
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom."
RL J. Protein Chem. 9:221-227(1990).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; C37196; C37196.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 11 AA; 1199 MW; 20B25813C7741777 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.2e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6
|
Db 1 Q 1

RESULT 14

BPP4_BOTIN

ID BPP4_BOTIN STANDARD; PRT; 11 AA.
AC P30424;
DT 01-APR-1993 (Rel. 25, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Bradykinin-potentiating peptide S4,1,2 (Angiotensin-converting
 DE enzyme inhibitor).
 OS Bothrops insularis (Island jararaca) (Queimada jararaca).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Bothrops.
 OX NCBI_TaxID=8723;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=90351557; PubMed=2386615;
 RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
 RT "Primary structure and biological activity of bradykinin potentiating
 RT peptides from Bothrops insularis snake venom."
 RL J. Protein Chem. 9:221-227(1990).
 CC -!- FUNCTION: This peptide both inhibits the activity of the
 CC angiotensin-converting enzyme and enhances the action of
 CC bradykinin by inhibiting the kinases that inactivate it.
 CC It acts as an indirect hypotensive agent.
 DR PIR; D37196; D37196.
 KW Hypotensive agent; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 11 AA; 1143 MW; 20BBBF13C7741777 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.2e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6
 |
 Db 1 Q 1

RESULT 15

BPPB_AGKHA

ID BPPB_AGKHA STANDARD; PRT; 11 AA.
 AC P01021;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Bradykinin-potentiating peptide B (Angiotensin-converting
 DE enzyme inhibitor).
 OS Agkistrodon halys blomhoffii (Mamushi) (Gloydus blomhoffii).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Gloydus.
 OX NCBI_TaxID=242054;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RA Kato H., Suzuki T.;
 RT "Amino acid sequence of bradykinin-potentiating peptide isolated from
 RT the venom of Agkistrodon halys blomhoffii."
 RL Proc. Jpn. Acad., B, Phys. Biol. Sci. 46:176-181(1970).
 CC -!- FUNCTION: This peptide both inhibits the activity of the

CC angiotensin-converting enzyme and enhances the action of
 CC bradykinin by inhibiting the kinases that inactivate it.
 CC It acts as an indirect hypotensive agent.
 DR PIR; A01254; XASNBA.
 KW Hypotensive agent; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 11 AA; 1199 MW; 295CBF0627741777 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.2e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6
 |
 Db 1 Q 1

RESULT 16

BPP AGKHP

ID BPP_AGKHP STANDARD; PRT; 11 AA.
 AC P04562;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Bradykinin-potentiating peptide (Angiotensin-converting
 DE enzyme inhibitor).
 OS Agkistrodon halys pallas (Chinese water mocassin) (Gloydus halys
 OS pallas).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Gloydus.
 OX NCBI_TaxID=8714;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=86177022; PubMed=3008123;
 RA Chi C.-W., Wang S.-Z., Xu L.-G., Wang M.-Y., Lo S.-S., Huang W.-D.;
 RT "Structure-function studies on the bradykinin potentiating peptide
 RT from Chinese snake venom (Agkistrodon halys pallas).";
 RL Peptides 6 Suppl. 3:339-342(1985).
 CC -!- FUNCTION: This peptide both inhibits the activity of the
 CC angiotensin-converting enzyme and enhances the action of
 CC bradykinin by inhibiting the kinases that inactivate it.
 CC It acts as an indirect hypotensive agent.
 DR PIR; JC0002; XAVIBH.
 KW Hypotensive agent; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 11 AA; 1112 MW; 30BABF1277686777 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.2e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6
 |
 Db 1 Q 1

RESULT 17

CA21_LITCI

ID CA21_LITCI STANDARD; PRT; 11 AA.
 AC P82087;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Caerulein 2.1/2.1Y4.
 OS Litoria citropa (Australian blue mountains tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
 OC Pelodryadinae; Litoria.
 OX NCBI_TaxID=94770;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RX MEDLINE=20057701; PubMed=10589099;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
 RT "Caerulein-like peptides from the skin glands of the Australian blue
 RT mountains tree frog Litoria citropa. Part 1. Sequence determination
 RT using electrospray mass spectrometry."
 RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
 CC -!- FUNCTION: Hypotensive neuropeptide (Probable).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
 CC -!- PTM: Isoform 2.1Y4 differs from isoform 2.1 in not being
 CC sulfated.
 CC -!- MASS SPECTROMETRY: MW=1372; METHOD=Electrospray.
 CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
 DR InterPro; IPR001651; Gastrin.
 DR PROSITE; PS00259; GASTRIN; FALSE_NEG.
 KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 4 4 SULFATION.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1312 MW; 10DAB7C4EDD861BB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 9.2e+04;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6

|

Db 1 Q 1

RESULT 18

CA22_LITCI

ID CA22_LITCI STANDARD; PRT; 11 AA.
 AC P82088;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Caerulein 2.2/2.2Y4.
 OS Litoria citropa (Australian blue mountains tree frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
 OC Pelodyadinae; Litoria.
 OX NCBI_TaxID=94770;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RX MEDLINE=20057701; PubMed=10589099;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
 RT "Caerulein-like peptides from the skin glands of the Australian blue
 RT mountains tree frog *Litoria citropa*. Part 1. Sequence determination
 RT using electrospray mass spectrometry."
 RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
 CC -!- FUNCTION: Hypotensive neuropeptide (Probable).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
 CC -!- PTM: Isoform 2.2Y4 differs from isoform 2.2 in not being
 CC sulfated.
 CC -!- MASS SPECTROMETRY: MW=1388; METHOD=Electrospray.
 CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
 DR InterPro; IPR001651; Gastrin.
 DR PROSITE; PS00259; GASTRIN; FALSE NEG.
 KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 4 4 SULFATION.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1328 MW; 10DAB894EDD861BB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.2e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6
 |
 Db 1 Q 1

RESULT 19

CA31_LITCI
 ID CA31_LITCI STANDARD; PRT; 11 AA.
 AC P82089;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Caerulein 3.1/3.1Y4.
 OS Litoria citropa (Australian blue mountains tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
 OC Pelodyadinae; Litoria.
 OX NCBI_TaxID=94770;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RX MEDLINE=20057701; PubMed=10589099;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
 RT "Caerulein-like peptides from the skin glands of the Australian blue

RT mountains tree frog *Litoria citropa*. Part 1. Sequence determination
 RT using electrospray mass spectrometry.";
 RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
 CC -!- FUNCTION: Hypotensive neuropeptide (Probable).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
 CC -!- PTM: Isoform 3.1Y4 differs from isoform 3.1 in not being
 CC sulfated.
 CC -!- MASS SPECTROMETRY: MW=1407; METHOD=Electrospray.
 CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
 DR InterPro; IPR001651; Gastrin.
 DR PROSITE; PS00259; GASTRIN; FALSE_NEG.
 KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 4 4 SULFATION.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1347 MW; 10DAB7D67861A86B CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.2e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6
 |
 Db 1 Q 1

RESULT 20

CA32_LITCI

ID CA32_LITCI STANDARD; PRT; 11 AA.
 AC P82090;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Caerulein 3.2/3.2Y4.
 OS *Litoria citropa* (Australian blue mountains tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
 OC Pelodyadinae; *Litoria*.
 OX NCBI_TaxID=94770;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RX MEDLINE=20057701; PubMed=10589099;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
 RT "Caerulein-like peptides from the skin glands of the Australian blue
 RT mountains tree frog *Litoria citropa*. Part 1. Sequence determination
 RT using electrospray mass spectrometry.";
 RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
 CC -!- FUNCTION: Hypotensive neuropeptide (Probable).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
 CC -!- PTM: Isoform 3.2Y4 differs from isoform 3.2 in not being
 CC sulfated.
 CC -!- MASS SPECTROMETRY: MW=1423; METHOD=Electrospray.
 CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.

DR InterPro; IPR001651; Gastrin.
 DR PROSITE; PS00259; GASTRIN; FALSE_NEG.
 KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 4 4 SULFATION.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1363 MW; 10DAB8867861A86B CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.2e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6
 |
 Db 1 Q 1

RESULT 21

CA41_LITCI
 ID CA41_LITCI STANDARD; PRT; 11 AA.
 AC P82091;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Caerulein 4.1/4.1Y4.
 OS Litoria citropa (Australian blue mountains tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
 OC Pelodyadinae; Litoria.
 OX NCBI_TaxID=94770;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RX MEDLINE=20057701; PubMed=10589099;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
 RT "Caerulein-like peptides from the skin glands of the Australian blue
 RT mountains tree frog Litoria citropa. Part 1. Sequence determination
 RT using electrospray mass spectrometry."
 RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
 CC -!- FUNCTION: Hypotensive neuropeptide (Probable).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
 CC -!- PTM: Isoform 4.1Y4 differs from isoform 4.1 in not being
 CC sulfated.
 CC -!- MASS SPECTROMETRY: MW=1388; METHOD=Electrospray.
 CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
 DR InterPro; IPR001651; Gastrin.
 DR PROSITE; PS00259; GASTRIN; FALSE_NEG.
 KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 4 4 SULFATION.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1328 MW; 10DAB7C4F5B861BB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 9.2e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6
|
Db 1 Q 1

RESULT 22

CA42_LITCI

ID CA42_LITCI STANDARD; PRT; 11 AA.
AC P82092;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Caerulein 4.2/4.2Y4.
OS Litoria citropa (Australian blue mountains tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
OC Pelodryadinae; Litoria.
OX NCBI_TaxID=94770;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RX MEDLINE=20057701; PubMed=10589099;
RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
RT "Caerulein-like peptides from the skin glands of the Australian blue
RT mountains tree frog Litoria citropa. Part 1. Sequence determination
RT using electrospray mass spectrometry."
RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
CC -!- FUNCTION: Hypotensive neuropeptide (Probable).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
CC -!- PTM: Isoform 4.2Y4 differs from isoform 4.2 in not being
CC sulfated.
CC -!- MASS SPECTROMETRY: MW=1404; METHOD=Electrospray.
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; FALSE_NEG.
KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 4 4 SULFATION.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1344 MW; 10DAB894F5B861BB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.2e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6
|
Db 1 Q 1

RESULT 23

CEP1_ACHFV

ID CEPl_ACHFU STANDARD; PRT; 11 AA.
AC P22790;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE Cardio-excitatory peptide-1 (ACEP-1).
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.
OX NCBI_TaxID=6530;
RN [1]
RP SEQUENCE.
RC STRAIN=Ferussac; TISSUE=Heart atrium;
RX MEDLINE=90211261; PubMed=2322251;
RA Fujimoto K., Ohta N., Yoshida M., Kubota I., Muneoka Y., Kobayashi M.;
RT "A novel cardio-excitatory peptide isolated from the atria of the
RT African giant snail, Achatina fulica.";
RL Biochem. Biophys. Res. Commun. 167:777-783(1990).
CC -!- FUNCTION: Potentiates the beat of the ventricle, and has also
CC excitatory actions on the penis retractor muscle, the buccal
CC muscle and the identified neurons controlling the buccal muscle
CC movement of achatina.
CC -!- SIMILARITY: TO POSSIBLE PEPTIDE L5 FROM APLYSIA.
DR PIR; A34662; A34662.
KW Hormone; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1305 MW; 82D6D5B9C7741365 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.2e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6
|
Db 3 Q 3

RESULT 24

CORZ_PERAM

ID CORZ_PERAM STANDARD; PRT; 11 AA.
AC P11496;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Corazonin.
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=89325572; PubMed=2753132;
RA Veenstra J.A.;
RT "Isolation and structure of corazonin, a cardioactive peptide from
RT the American cockroach.";

RL FEBS Lett. 250:231-234(1989).
 CC -!- FUNCTION: Cardioactive peptide. Corazonin is probably involved
 CC in the physiological regulation of the heart beat.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 DR PIR; S05002; S05002.
 KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1387 MW; C7CFF32D6415AB46 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.2e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6
 |
 Db 1 Q 1

RESULT 25

COXA_CANFA

ID COXA_CANFA STANDARD; PRT; 11 AA.
 AC P99501;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Cytochrome c oxidase polypeptide Va (EC 1.9.3.1) (Fragment).
 GN COX5A.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Heart;
 RX MEDLINE=98163340; PubMed=9504812;
 RA Dunn M.J., Corbett J.M., Wheeler C.H.;
 RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
 RT dog heart proteins."
 RL Electrophoresis 18:2795-2802(1997).
 CC -!- FUNCTION: This is the heme A-containing chain of cytochrome c
 CC oxidase, the terminal oxidase in mitochondrial electron transport.
 CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
 CC c + 2 H(2)O.
 CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
 CC -!- SIMILARITY: Belongs to the cytochrome c oxidase Va family.
 DR HSC-2DPAGE; P99501; DOG.
 DR InterPro; IPR003204; Cyt_c_ox5A.
 DR Pfam; PF02284; COX5A; 1.
 KW Oxidoreductase; Heme; Mitochondrion; Inner membrane.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1274 MW; 910B35C5B1AB11F5 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.2e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 E 4
|
Db 6 E 6

RESULT 26

CSI5_BACSU

ID CSI5_BACSU STANDARD; PRT; 11 AA.
AC P81095;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cold shock protein CSI5 (11 kDa cold shock protein) (Fragment).
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE.
RC STRAIN=168 / JH642;
RA Graumann P.L., Schmid R., Marahiel M.A.;
RL Submitted (OCT-1997) to Swiss-Prot.
RN [2]
RP CHARACTERIZATION.
RC STRAIN=168 / JH642;
RX MEDLINE=96345629; PubMed=8755892;
RA Graumann P., Schroeder K., Schmid R., Marahiel M.A.;
RT "Cold shock stress-induced proteins in Bacillus subtilis."
RL J. Bacteriol. 178:4611-4619(1996).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- INDUCTION: In response to low temperature.
CC -!- CAUTION: Could not be found in the genome of B.subtilis 168.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1360 MW; 15F6ECEE6322C330 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.2e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 R 5
|
Db 2 R 2

RESULT 27

CX5A_CONAL

ID CX5A_CONAL STANDARD; PRT; 11 AA.
AC P58848;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Conotoxin au5a.
OS Conus aulicus (Court cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=89437;
RN [1]

RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
 RC TISSUE=Venom;
 RX MEDLINE=99452958; PubMed=10521453;
 RA Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,
 RA Hooper D., Shetty R., Delacruz R.C., Nielsen J.S., Zhou L.M.,
 RA Bandyopadhyay P., Craig A.G., Olivera B.M.;
 RT "The T-superfamily of conotoxins."
 RL J. Biol. Chem. 274:30664-30671(1999).
 RN [2]
 RP ERRATUM.
 RA Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,
 RA Hooper D., Shetty R., Delacruz R.C., Nielsen J.S., Zhou L.M.,
 RA Bandyopadhyay P., Craig A.G., Olivera B.M.;
 RL J. Biol. Chem. 274:36030-36030(1999).
 CC -!- FUNCTION: Causes dorsal fins drooping in fish. No effect is
 CC observed when injected into mice.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -!- MASS SPECTROMETRY: MW=1436.6; METHOD=LSIMS.
 CC -!- SIMILARITY: Belongs to the conotoxin T-superfamily.
 DR PIR; A59146; A59146.
 KW Toxin.
 FT DISULFID 2 9
 FT DISULFID 3 10
 SQ SEQUENCE 11 AA; 1441 MW; 21A36775440059D7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.2e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 R 5
 |
 Db 7 R 7

RESULT 28

CX5B_CONAL

ID CX5B_CONAL STANDARD; PRT; 11 AA.
 AC P58849;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Conotoxin au5b.
 OS Conus aulicus (Court cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=89437;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Venom;
 RX MEDLINE=99452958; PubMed=10521453;
 RA Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,
 RA Hooper D., Shetty R., Delacruz R.C., Nielsen J.S., Zhou L.M.,
 RA Bandyopadhyay P., Craig A.G., Olivera B.M.;
 RT "The T-superfamily of conotoxins."
 RL J. Biol. Chem. 274:30664-30671(1999).

RN [2]
 RP ERRATUM.
 RA Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,
 RA Hooper D., Shetty R., DelaCruz R.C., Nielsen J.S., Zhou L.M.,
 RA Bandyopadhyay P., Craig A.G., Olivera B.M.;
 RL J. Biol. Chem. 274:36030-36030(1999).
 CC -!- FUNCTION: Causes dorsal fins drooping in fish. No effect is
 CC observed when injected into mice (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -!- MASS SPECTROMETRY: MW=1388.6; METHOD=LSIMS.
 CC -!- SIMILARITY: Belongs to the conotoxin T-superfamily.
 DR PIR; B59146; B59146.
 KW Toxin.
 FT DISULFID 2 9
 FT DISULFID 3 10
 SQ SEQUENCE 11 AA; 1393 MW; 21A36775440042D7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.2e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 R 5
 |
 Db 7 R 7

RESULT 29

CXL1_CONMR

ID CXL1_CONMR STANDARD; PRT; 11 AA.
 AC P58807;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Lambda-conotoxin CMrVIA.
 OS Conus marmoreus (Marble cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=42752;
 RN [1]
 RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
 RC TISSUE=Venom;
 RX MEDLINE=20564325; PubMed=10988292;
 RA Balaji R.A., Ohtake A., Sato K., Gopalakrishnakone P., Kini R.M.,
 RA Seow K.T., Bay B.-H.;
 RT "Lambda-conotoxins, a new family of conotoxins with unique disulfide
 RT pattern and protein folding. Isolation and characterization from the
 RT venom of Conus marmoreus."
 RL J. Biol. Chem. 275:39516-39522(2000).
 CC -!- FUNCTION: Inhibits the neuronal noradrenaline transporter.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -!- MASS SPECTROMETRY: MW=1237.93; MW_ERR=0.21; METHOD=Electrospray.
 CC -!- SIMILARITY: Belongs to the chi/lambda-conotoxin family.
 KW Neurotoxin; Toxin; Hydroxylation.
 FT DISULFID 2 11

FT DISULFID 3 8
FT MOD_RES 10 10 HYDROXYLATION.
SQ SEQUENCE 11 AA; 1226 MW; 277AAC60B7232B58 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.2e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 K 2
|
Db 6 K 6

RESULT 30

EFG_CLOPA

ID EFG_CLOPA STANDARD; PRT; 11 AA.
AC P81350;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Elongation factor G (EF-G) (CP 5) (Fragment).
GN FUSA.
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]
RP SEQUENCE.
RC STRAIN=W5;
RX MEDLINE=98291870; PubMed=9629918;
RA Flengsrud R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
RT sequence analysis of proteins from Clostridium pasteurianum W5."
RL Electrophoresis 19:802-806(1998).
CC -!- FUNCTION: This protein promotes the GTP-dependent translocation of
CC the nascent protein chain from the A-site to the P-site of the
CC ribosome.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the GTP-binding elongation factor family.
CC EF-G/EF-2 subfamily.
DR InterPro; IPR000795; EF_GTPbind.
DR PROSITE; PS00301; EFACTOR_GTP; PARTIAL.
KW Elongation factor; Protein biosynthesis; GTP-binding.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1337 MW; 412E71F1D9C33B17 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.2e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 K 2
|
Db 1 K 1

RESULT 31

ES1_RAT

ID ES1_RAT STANDARD; PRT; 11 AA.
AC P56571;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE ES1 protein, mitochondrial (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RC STRAIN=Wistar; TISSUE=Heart;
RA Li X.-P., Pleissner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,
RA Jungblut P.R.;
RL Submitted (SEP-1998) to Swiss-Prot.
CC -!- SUBCELLULAR LOCATION: Mitochondrial (Potential).
CC -!- MISCELLANEOUS: By 2D-PAGE, the determined pI of this protein (spot
CC P2) is: 8.9, its MW is: 25 kDa.
CC -!- SIMILARITY: BELONGS TO THE ES1 FAMILY.
KW Mitochondrion.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1142 MW; D862272D32C72DC2 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.2e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 R 5
|
Db 1 R 1

RESULT 32

FAR6_PENMO

ID FAR6_PENMO STANDARD; PRT; 11 AA.
AC P83321;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRFamide-like neuropeptide FLP6 (DGRTPALRLRF-amide).
OS Penaeus monodon (Penaeid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RX MEDLINE=21956277; PubMed=11959015;
RA Sithigorngul P., Pupuem J., Krungkasem C., Longyant S.,
RA Chaivisuthangkura P., Sithigorngul W., Petsom A.;
RT "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk
RT of the giant tiger prawn Penaeus monodon."
RL Comp. Biochem. Physiol. 131B:325-337(2002).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=1301.8; METHOD=MALDI.

CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC family.
DR GO; GO:0007218; P:neuropeptide signaling pathway; TAS.
KW Neuropeptide; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1301 MW; 9A19C860072DC771 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.2e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 D 9
|
Db 1 D 1

RESULT 33

FAR9_CALVO

ID FAR9_CALVO STANDARD; PRT; 11 AA.
AC P41864;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CalliFMRFamide 9.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Rehfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT neuropeptides (designated calliFMRFamides) from the blowfly
RT Calliphora vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC family.
DR PIR; I41978; I41978.
KW Neuropeptide; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1359 MW; 8160CE46CAA44321 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.2e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 K 2
|
Db 5 K 5

RESULT 34

HS70_PINPS

ID HS70_PINPS STANDARD; PRT; 11 AA.
AC P81672;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Heat shock 70 kDa protein (Fragment).
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=71647;
RN [1]
RP SEQUENCE.
RC TISSUE=Needle;
RX MEDLINE=99274088; PubMed=10344291;
RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins.";
RL Electrophoresis 20:1098-1108(1999).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this protein
CC (spot N164) is: 5.4, its MW is: 73 kDa.
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
KW ATP-binding; Heat shock; Multigene family.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1228 MW; 037C1BE8DAA44DD0 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.2e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 E 4
|
Db 2 E 2

RESULT 35

LADD_ONCMY

ID LADD_ONCMY STANDARD; PRT; 11 AA.
AC P81018;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Ladderlectin (Fragment).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE.
RC TISSUE=Blood;
RX MEDLINE=97293418; PubMed=9149391;
RA Jensen L.E., Thiel S., Petersen T.E., Jensenuis J.C.;
RT "A rainbow trout lectin with multimeric structure.";
RL Comp. Biochem. Physiol. 116B:385-390(1997).
CC -!- FUNCTION: Lectin that binds sepharose.

CC -!- COFACTOR: Calcium is essential for sepharose binding.
CC -!- SUBUNIT: Multimeric.
KW Lectin; Calcium.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1163 MW; 0B26227FF6D45404 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.2e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
|
Db 1 A 1

RESULT 36

LPW_THETH

ID LPW_THETH STANDARD; PRT; 11 AA.
AC P05624;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Trp operon leader peptide.
GN TRPL.
OS Thermus thermophilus.
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OC Thermus.
OX NCBI_TaxID=274;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HB8 / ATCC 27634;
RX MEDLINE=89000781; PubMed=2844259;
RA Sato S., Nakada Y., Kanaya S., Tanaka T.;
RT "Molecular cloning and nucleotide sequence of Thermus thermophilus
RT HB8 trpE and trpG."
RL Biochim. Biophys. Acta 950:303-312(1988).
CC -!- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS
CC OF TRYPTOPHAN.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).

DR EMBL; X07744; CAA30565.1; -.
KW Tryptophan biosynthesis; Leader peptide.
SQ SEQUENCE 11 AA; 1228 MW; 364B295A772DC5A7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.2e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
|

Db 2 A 2

RESULT 37

LSK1_LEUMA

ID LSK1_LEUMA STANDARD; PRT; 11 AA.
AC P04428;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Leucosulfakinin-I (LSK-I).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE.
RX MEDLINE=86315858; PubMed=3749893;
RA Nachman R.J., Holman G.M., Haddon W.F., Ling N.;
RT "Leucosulfakinin, a sulfated insect neuropeptide with homology to
RT gastrin and cholecystokinin.";
RL Science 234:71-73(1986).
CC -!- FUNCTION: Change the frequency and amplitude of contractions of
CC the hindgut. Inhibits muscle contraction of hindgut.
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
DR PIR; A01622; GMROL.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; 1.
KW Hormone; Amidation; Sulfation.
FT MOD_RES 6 6 SULFATION.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1459 MW; 7E4E0680E86B5AAB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.2e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 E 4
|
Db 1 E 1

RESULT 38

LSKP_PERAM

ID LSKP_PERAM STANDARD; PRT; 11 AA.
AC P36885;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Perisulfakinin (Pea-SK-I).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]

RP SEQUENCE.
 RC TISSUE=Corpora cardiaca;
 RX MEDLINE=90137190; PubMed=2615921;
 RA Veenstra J.A.;
 RT "Isolation and structure of two gastrin/CCK-like neuropeptides from
 RT the American cockroach homologous to the leucosulfakinins.";
 RL Neuropeptides 14:145-149(1989).
 CC -!- FUNCTION: Stimulates hindgut contractions.
 CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
 DR PIR; A60656; A60656.
 DR InterPro; IPR001651; Gastrin.
 DR PROSITE; PS00259; GASTRIN; 1.
 KW Hormone; Amidation; Sulfation.
 FT MOD_RES 6 6 SULFATION.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1445 MW; 8B4E0680E86B5AAA CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.2e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 E 4
 |
 Db 1 E 1

RESULT 39

MHBI_KLEPN

ID MHBI_KLEPN STANDARD; PRT; 11 AA.
 AC P80580;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Maleylpyruvate isomerase (EC 5.2.1.4) (Fragment).
 GN MHBI.
 OS Klebsiella pneumoniae.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Klebsiella.
 OX NCBI_TaxID=573;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=96349117; PubMed=8760924;
 RA Robson N.D., Parrott S., Cooper R.A.;
 RT "In vitro formation of a catabolic plasmid carrying Klebsiella
 RT pneumoniae DNA that allows growth of Escherichia coli K-12 on 3-
 RT hydroxybenzoate.";
 RL Microbiology 142:2115-2120(1996).
 CC -!- CATALYTIC ACTIVITY: 3-maleylpyruvate = 3-fumarylpyruvate.
 KW Isomerase.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1387 MW; 1EE0E2DD49C9D5AB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.2e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 K 2

Db |
 2 K 2

RESULT 40

MLG_THETS

ID MLG_THETS STANDARD; PRT; 11 AA.
AC P41989;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Melanotropin gamma (Gamma-melanocyte stimulating hormone) (Gamma-MSH).
OS Theromyzon tessulatum (Leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC Rhynchobdellida; Glossiphoniidae; Theromyzon.
OX NCBI_TaxID=13286;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=94298944; PubMed=8026574;
RA Salzet M., Wattez C., Bulet P., Malecha J.;
RT "Isolation and structural characterization of a novel peptide related
RT to gamma-melanocyte stimulating hormone from the brain of the leech
RT Theromyzon tessulatum."
RL FEBS Lett. 348:102-106(1994).
CC -!- SIMILARITY: Belongs to the POMC family.
DR PIR; S45698; S45698.
KW Hormone; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1486 MW; 2DB8FACE6409C1E8 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.2e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 K 2
 |
Db 10 K 10

RESULT 41

MORN_HUMAN

ID MORN_HUMAN STANDARD; PRT; 11 AA.
AC P01163;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Morphogenetic neuropeptide (Head activator) (HA).
OS Homo sapiens (Human),
OS Rattus norvegicus (Rat),
OS Bos taurus (Bovine),
OS Anthopleura elegantissima (Sea anemone), and
OS Hydra attenuata (Hydra) (Hydra vulgaris).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606, 10116, 9913, 6110, 6087;
RN [1]

RP SEQUENCE.
RC SPECIES=Human, Rat, and Bovine;
RX MEDLINE=82035850; PubMed=7290191;
RA Bodenmuller H., Schaller H.C.;
RT "Conserved amino acid sequence of a neuropeptide, the head activator,
RT from coelenterates to humans.";
RL Nature 293:579-580(1981).
RN [2]
RP SEQUENCE.
RC SPECIES=A.elegantissima, and H.attenuata;
RA Schaller H.C., Bodenmuller H.;
RT "Isolation and amino acid sequence of a morphogenetic peptide from
RT hydra.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7000-7004(1981).
RN [3]
RP SYNTHESIS.
RX MEDLINE=82050803; PubMed=7297679;
RA Birr C., Zachmann B., Bodenmuller H., Schaller H.C.;
RT "Synthesis of a new neuropeptide, the head activator from hydra.";
RL FEBS Lett. 131:317-321(1981).
RN [4]
RP FUNCTION.
RX MEDLINE=90059923; PubMed=2583101;
RA Schaller H.C., Druffel-Augustin S., Dubel S.;
RT "Head activator acts as an autocrine growth factor for NH15-CA2 cells
RT in the G2/mitosis transition.";
RL EMBO J. 8:3311-3318(1989).
CC -!- FUNCTION: HA acts as an autocrine growth factor for neural cells
CC in the G2/mitosis transition.
CC -!- CAUTION: This peptide was first isolated from nerve cells of hydra
CC and was called head activator by the authors, because it induced
CC head-specific growth and differentiation in this animal. It has
CC been found in mammalian intestine and hypothalamus.
DR PIR; A01427; YHRT.
DR PIR; A93900; YHXAE.
DR PIR; B01427; YHHU.
DR PIR; B93900; YHJFHY.
DR PIR; C01427; YHBO.
DR GK; P01163; -.
KW Growth factor; Cell cycle; Mitosis; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 11 AA; 1142 MW; 37927417C325B878 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.2e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6
|
Db 1 Q 1

RESULT 42
NUHM_CANFA
ID NUHM_CANFA STANDARD; PRT; 11 AA.
AC P49820;
DT 01-OCT-1996 (Rel. 34, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE NADH-ubiquinone oxidoreductase 24 kDa subunit (EC 1.6.5.3)
 DE (EC 1.6.99.3) (Fragment).
 GN NDUFV2.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Heart;
 RX MEDLINE=98163340; PubMed=9504812;
 RA Dunn M.J., Corbett J.M., Wheeler C.H.;
 RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
 RT dog heart proteins.";
 RL Electrophoresis 18:2795-2802(1997).
 CC -!- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY
 CC CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED
 CC TO BE UBIQUINONE. COMPONENT OF THE FLAVOPROTEIN-SULFUR (FP)
 CC FRAGMENT OF THE ENZYME.
 CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
 CC -!- CATALYTIC ACTIVITY: NADH + acceptor = NAD(+) + reduced acceptor.
 CC -!- COFACTOR: Binds 1 2Fe-2S cluster (Potential).
 CC -!- SUBUNIT: Mammalian complex I is composed of 45 different subunits.
 CC -!- SUBCELLULAR LOCATION: Matrix and cytoplasmic side of the
 CC mitochondrial inner membrane.
 CC -!- SIMILARITY: Belongs to the complex I 24 kDa subunit family.
 DR HSC-2DPAGE; P49820; DOG.
 DR InterPro; IPR002023; Cmplx1_24kDa.
 DR PROSITE; PS01099; COMPLEX1_24K; PARTIAL.
 KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Metal-binding;
 KW Iron-sulfur; Iron; 2Fe-2S.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1099 MW; 267F5369C9C72DD8 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.2e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
 |
 Db 2 A 2

RESULT 43

OAIF_SARBU

ID OAIF_SARBU STANDARD; PRT; 11 AA.
 AC P83518;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ovary-derived ACE interactive factor (Neb-ODAIF) [Contains: Neb-
 DE ODAIF(1-9); Neb-ODAIF(1-7)].
 OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;

OC Sarcophagidae; Sarcophaga.
 OX NCBI_TaxID=7385;
 RN [1]
 RP SEQUENCE, SYNTHESIS, CHARACTERIZATION, AND MASS SPECTROMETRY.
 RC TISSUE=Ovary;
 RX MEDLINE=22272747; PubMed=12383874;
 RA Vandingenen A., Hens K., Baggerman G., Macours N., Schoofs L.,
 RA De Loof A., Huybrechts R.;
 RT "Isolation and characterization of an angiotensin converting enzyme
 RT substrate from vitellogenic ovaries of *Neobellieria bullata*.";
 RL Peptides 23:1853-1863(2002).
 CC -!- FUNCTION: Substrate for angiotensin converting enzyme (ACE) in
 CC vitro.
 CC -!- PTM: ACE hydrolyzes Neb-ODAIF by sequentially cleaving off two C-
 CC terminal dipeptides.
 CC -!- MASS SPECTROMETRY: MW=1312.7; METHOD=MALDI; RANGE=1-11.
 CC -!- SIMILARITY: To the N-terminal part of insect vitellogenins.
 FT PEPTIDE 1 11 NEB-ODAIF.
 FT PEPTIDE 1 9 NEB-ODAIF(1-9).
 FT PEPTIDE 1 7 NEB-ODAIF(1-7).
 SQ SEQUENCE 11 AA; 1314 MW; 4E114BB566C5A763 CRC64;

 Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.2e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 2 K 2
 |
 Db 2 K 2

RESULT 44
 PVK1_PERAM
 ID PVK1_PERAM STANDARD; PRT; 11 AA.
 AC P41837;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Periviscerokinin-1 (Pea-PVK-1).
 OS Periplaneta americana (American cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
 OC Blattidae; Periplaneta.
 OX NCBI_TaxID=6978;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Abdominal perisymphathetic organs;
 RX MEDLINE=95232021; PubMed=7716075;
 RA Predel R., Linde D., Rapus J., Vettermann S., Penzlin H.;
 RT "Periviscerokinin (Pea-PVK): a novel myotropic neuropeptide from the
 RT perisymphathetic organs of the American cockroach.";
 RL Peptides 16:61-66(1995).
 CC -!- FUNCTION: MYOACTIVE PEPTIDE; HAS EXCITORY ACTIONS ON THE
 CC HYPERNEURAL MUSCLE.
 KW Neuropeptide; Amidation.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1114 MW; 39DB5419D7605728 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.2e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
|
Db 2 A 2

RESULT 45

RANC_RANPI

ID RANC_RANPI STANDARD; PRT; 11 AA.
AC P08951;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ranatensin-C.
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8404;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=84131098; PubMed=6141890;
RA Nakajima T.;
RL Unpublished results, cited by:
RL Erspamer V., Erspamer G.F., Mazzanti G., Endean R.;
RL Comp. Biochem. Physiol. 77C:99-108(1984).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the bombesin/neuromedin B/ranatensin
CC family.
DR InterPro; IPR000874; Bombesin.
DR Pfam; PF02044; Bombesin; 1.
DR PROSITE; PS00257; BOMBESIN; 1.
KW Amphibian defense peptide; Bombesin family; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1304 MW; D6C9885A61ADC366 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.2e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 T 10
|
Db 2 T 2

RESULT 46

RE41_LITRU

ID RE41_LITRU STANDARD; PRT; 11 AA.
AC P82074;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Rubellidin 4.1.
 OS *Litoria rubella* (Desert tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
 OC Pelodryadinae; *Litoria*.
 OX NCBI_TaxID=104895;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
 RA Tyler M.J., Wallace J.C.;
 RT "The structure of new peptides from the Australian red tree frog
 RT '*Litoria rubella*'. The skin peptide profile as a probe for the study
 RT of evolutionary trends of amphibians."
 RL Aust. J. Chem. 49:955-963(1996).
 CC -!- FUNCTION: Shows neither neuropeptide activity nor antibiotic
 CC activity.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
 CC -!- MASS SPECTROMETRY: MW=1039; METHOD=FAB.
 KW Amphibian defense peptide; Amidation.
 FT MOD RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1040 MW; 84ED5CBC2877205A CRC64;

 Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.2e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 D 9
 |
 Db 4 D 4

RESULT 47
 RR2_CONAM
 ID RR2 CONAM STANDARD; PRT; 11 AA.
 AC P42341;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Chloroplast 30S ribosomal protein S2 (Fragment).
 GN RPS2.
 OS *Conopholis americana* (Squawroot).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC lamiids; Lamiales; Orobanchaceae; Orobancheae; *Conopholis*.
 OX NCBI_TaxID=4179;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92145776; PubMed=1723664;
 RA Taylor G., Wolfe K.H., Morden C.W., Depamphilis C.W., Palmer J.D.;
 RT "Lack of a functional plastid tRNA(Cys) gene is associated with loss
 RT of photosynthesis in a lineage of parasitic plants."
 RL Curr. Genet. 20:515-518(1991).
 CC -!- SIMILARITY: Belongs to the S2P family of ribosomal proteins.
 CC -----

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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DR EMBL; X64567; CAA45868.1; -.
DR PIR; S32575; S32575.
DR HAMAP; MF_00291; -; 1.
DR InterPro; IPR001865; Ribosomal_S2.
DR PROSITE; PS00962; RIBOSOMAL_S2_1; PARTIAL.
DR PROSITE; PS00963; RIBOSOMAL_S2_2; PARTIAL.
KW Ribosomal protein; Chloroplast.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1497 MW; 76CD719954536B44 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.2e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 E 4
|
Db 11 E 11

RESULT 48

RRPL_CHAV

ID RRPL_CHAV STANDARD; PRT; 11 AA.
AC P13179;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE RNA polymerase beta subunit (EC 2.7.7.48) (Large structural protein)
DE (L protein) (Fragment).
GN L.
OS Chandipura virus (strain I653514).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Vesiculovirus.
OX NCBI_TaxID=11273;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89299473; PubMed=2741347;
RA Masters P.S., Bhella R.S., Butcher M., Patel B., Ghosh H.P.,
RA Banerjee A.K.;
RT "Structure and expression of the glycoprotein gene of Chandipura
RT virus.";
RL Virology 171:285-290(1989).
CC -!- FUNCTION: THIS PROTEIN IS PROBABLY A COMPONENT OF THE ACTIVE
CC POLYMERASE. IT MAY FUNCTION IN RNA SYNTHESIS, CAPPING, AS WELL AS
CC METHYLATION OF CAPS, AND POLY(A) SYNTHESIS.
CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC {RNA} (N).
CC -!- SUBUNIT: THOUGHT TO FORM A TRANSCRIPTION COMPLEX WITH THE
CC NUCLEOCAPSID (N) PROTEIN.
CC -!- SIMILARITY: WITH THE L PROTEIN OF OTHER RHABDOVIRUSES AND

CC PARAMYXOVIRUSES.

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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J04350; AAA42917.1; -.
KW Transferase; RNA-directed RNA polymerase.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1189 MW; 0335D6E3AAB2D764 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.2e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 D 9
|
Db 2 D 2

RESULT 49

RS30_ONCMY

ID RS30_ONCMY STANDARD; PRT; 11 AA.
AC P83328;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE 40S ribosomal protein S30 (Fragment).
GN FAU.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Skin mucus;
RX MEDLINE=22142142; PubMed=12147245;
RA Fernandes J.M.O., Smith V.J.;
RT "A novel antimicrobial function for a ribosomal peptide from rainbow
RT trout skin."
RL Biochem. Biophys. Res. Commun. 296:167-171(2002).
CC -!- FUNCTION: Has antibacterial activity against Gram-positive
CC bacteria.
CC -!- MASS SPECTROMETRY: MW=6676.6; METHOD=MALDI.
CC -!- SIMILARITY: Belongs to the S30E family of ribosomal proteins.
KW Ribosomal protein; Antibiotic.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1123 MW; 2312AB630DD735B8 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.2e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 K 2
|
Db 1 K 1

RESULT 50

T2P1_PROVU

ID T2P1_PROVU STANDARD; PRT; 11 AA.
AC P31031;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Type II restriction enzyme PvuI (EC 3.1.21.4) (Endonuclease PvuI)
DE (R.PvuI) (Fragment).
GN PVUIR.
OS Proteus vulgaris.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Proteus.
OX NCBI_TaxID=585;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13315;
RX MEDLINE=93087186; PubMed=1454536;
RA Smith M.D., Longo M., Gerard G.F., Chatterjee D.K.;
RT "Cloning and characterization of genes for the PvuI restriction and
RT modification system.";
RL Nucleic Acids Res. 20:5743-5747(1992).
CC -!- FUNCTION: RECOGNIZES THE DOUBLE-STRANDED SEQUENCE CGATCG AND
CC CLEAVES AFTER T-4.
CC -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage of DNA to give
CC specific double-stranded fragments with terminal 5'-phosphates.
CC -----
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CC -----
DR EMBL; L04163; AAA25660.1; -.
DR PIR; S35490; S35490.
DR REBASE; 1541; PvuI.
KW Restriction system; Hydrolase; Nuclease; Endonuclease.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1300 MW; 9F0CDE7955B72B1A CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.2e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 D 9
|
Db 4 D 4

RESULT 51

TIN1_HOPTI

ID TIN1_HOPTI STANDARD; PRT; 11 AA.
 AC P82651;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Tigerinin-1.
 OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae;
 OC Hoplobatrachus.
 OX NCBI_TaxID=103373;
 RN [1]
 RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.
 RC TISSUE=Skin secretion;
 RX PubMed=11031261;
 RA Purna Sai K., Jaganadham M.V., Vairamani M., Raju N.P.,
 RA Devi A.S., Nagaraj R., Sitaram N.;
 RT "Tigerinins: novel antimicrobial peptides from the Indian frog Rana
 RT tigerina.";
 RL J. Biol. Chem. 276:2701-2707(2001).
 CC -!- FUNCTION: Antibacterial activity against B.subtilis, E.coli,
 CC S.aureus, M.luteus, P.putida and S.cerevisiae.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- MASS SPECTROMETRY: MW=1342; METHOD=MALDI.
 KW Amphibian defense peptide; Antibiotic; Fungicide; Amidation.
 FT DISULFID 2 10
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1344 MW; A2087DC960476056 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.2e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 R 5
 |
 Db 9 R 9

RESULT 52

TIN4_HOPTI

ID TIN4_HOPTI STANDARD; PRT; 11 AA.
 AC P82654;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Tigerinin-4.
 OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae;
 OC Hoplobatrachus.
 OX NCBI_TaxID=103373;
 RN [1]
 RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.
 RC TISSUE=Skin secretion;

RX PubMed=11031261;
 RA Purna Sai K., Jaganadham M.V., Vairamani M., Raju N.P.,
 RA Devi A.S., Nagaraj R., Sitaram N.;
 RT "Tigerinins: novel antimicrobial peptides from the Indian frog *Rana*
 RT *tigerina*.";
 RL J. Biol. Chem. 276:2701-2707(2001).
 CC -!- FUNCTION: Antibacterial activity against *B.subtilis*, *E.coli*,
 CC *S.aureus*, *M.luteus*, *P.putida* and *S.cerevisiae*.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- MASS SPECTROMETRY: MW=1247; METHOD=MALDI.
 KW Amphibian defense peptide; Antibiotic.
 FT DISULFID 3 11
 SQ SEQUENCE 11 AA; 1248 MW; 117D8EFD37605DCB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.2e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 R 5
 |
 Db 1 R 1

RESULT 53

TKC2_CALVO

ID TKC2_CALVO STANDARD; PRT; 11 AA.
 AC P41518;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Callitachykinin II.
 OS Calliphora vomitoria (Blue blowfly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 OC Calliphoridae; Calliphora.
 OX NCBI_TaxID=27454;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RX MEDLINE=95075727; PubMed=7984492;
 RA Lundquist C.T., Clottens F.L., Holman G.M., Nichols R., Nachman R.J.,
 RA Naessel D.R.;
 RT "Callitachykinin I and II, two novel myotropic peptides isolated from
 RT the blowfly, *Calliphora vomitoria*, that have resemblances to
 RT tachykinins.";
 RL Peptides 15:761-768(1994).
 CC -!- FUNCTION: Myoactive peptide.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
 KW Tachykinin; Neuropeptide; Amidation.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1103 MW; 15D7E3F9C9CDD444 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.2e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
|
Db 6 A 6

RESULT 54

TKN1_PSEGU

ID TKN1_PSEGU STANDARD; PRT; 11 AA.
AC P42986;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Kassinin-like peptide K-I (PG-KI).
OS Pseudophryne guentheri (Guenther's toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
OC Myobatrachinae; Pseudophryne.
OX NCBI_TaxID=30349;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=90287814; PubMed=2356157;
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RA Roberts J.D., Melchiorri P., Erspamer V.;
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
RT the Australian frog Pseudophryne guentheri.";
RL Peptides 11:299-304(1990).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR PIR; B60409; B60409.
DR InterPro; IPR002040; Tachy Neurokinin.
DR InterPro; IPR008215; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1269 MW; 3DBA7C37C9CB1AB7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.2e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6
|
Db 1 Q 1

RESULT 55

TKN1_UPEIN

ID TKN1_UPEIN STANDARD; PRT; 11 AA.
AC P82026;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Uperin 1.1.
OS Uperoleia inundata (Floodplain toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
OC Myobatrachinae; Uperoleia.
OX NCBI_TaxID=104953;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RA Bradford A.M., Raftery M.J., Bowie J.H., Tyler M.J., Wallace J.C.,
RA Adams G.W., Severini C.;
RT "Novel uperin peptides from the dorsal glands of the australian
RT floodplain toadlet Uperoleia inundata.";
RL Aust. J. Chem. 49:475-484(1996).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
CC -!- MASS SPECTROMETRY: MW=1208; METHOD=FAB.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR Pfam; PF02202; Tachykinin; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1226 MW; 3293693E59CDD457 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.2e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6
|
Db 1 Q 1

RESULT 56

TKN1_UPERU
ID TKN1_UPERU STANDARD; PRT; 11 AA.
AC P08612;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Uperolein.
OS Uperoleia rugosa (Wrinkled toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
OC Myobatrachinae; Uperoleia.

OX NCBI_TaxID=8368;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=75131227; PubMed=1120493;
 RA Anastasi A., Erspamer V., Endean R.;
 RT "Structure of uperolein, a physalaemin-like endecapeptide occurring
 in the skin of Uperoleia rugosa and Uperoleia marmorata.";
 RL Experientia 31:394-395(1975).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR InterPro; IPR008215; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1252 MW; 32867C3E59CDD457 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.2e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6
 |
 Db 1 Q 1

RESULT 57

TKN2_PSEGU

ID TKN2_PSEGU STANDARD; PRT; 11 AA.
 AC P42987;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Kassinin-like peptide K-II (PG-KII).
 OS Pseudophryne guentheri (Guenther's toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
 OC Myobatrachinae; Pseudophryne.
 OX NCBI_TaxID=30349;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=90287814; PubMed=2356157;
 RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
 RA Roberts J.D., Melchiorri P., Erspamer V.;
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of
 the Australian frog Pseudophryne guentheri.";

RL Peptides 11:299-304(1990).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; C60409; C60409.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR InterPro; IPR008215; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1246 MW; 3A247C37C9CB1AB7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.2e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6
 |
 Db 1 Q 1

RESULT 58

TKN2_UPERU
 ID TKN2_UPERU STANDARD; PRT; 11 AA.
 AC P08616;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Rugosauperolein II ([Lys5,Thr6]physalaemin).
 OS Uperoleia rugosa (Wrinkled toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
 OC Myobatrachinae; Uperoleia.
 OX NCBI_TaxID=8368;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=80223080; PubMed=7389029;
 RA Nakajima T., Yasuhara T., Erspamer V., Erspamer G.F., Negri L.;
 RT "Physalaemin- and bombesin-like peptides in the skin of the
 RT Australian leptodactylid frog Uperoleia rugosa."
 RL Chem. Pharm. Bull. 28:689-695(1980).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the tachykinin family.

DR InterPro; IPR002040; Tachy_Neurokinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1270 MW; 3293693E59D1A327 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.2e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6
 |
 Db 1 Q 1

RESULT 59

TKN3_PSEGU

ID TKN3_PSEGU STANDARD; PRT; 11 AA.
 AC P42988;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Kassinin-like peptide K-III (PG-KIII).
 OS Pseudophryne guentheri (Guenther's toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
 OC Myobatrachinae; Pseudophryne.
 OX NCBI_TaxID=30349;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=90287814; PubMed=2356157;
 RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
 RA Roberts J.D., Melchiorri P., Erspamer V.;
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of
 RT the Australian frog Pseudophryne guentheri.";
 RL Peptides 11:299-304(1990).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; D60409; D60409.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR InterPro; IPR008215; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.

SQ SEQUENCE 11 AA; 1268 MW; 3DBA7C37C9CB1457 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.2e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6

Db 1 Q 1

RESULT 60

TKN4_PSEGU

ID TKN4_PSEGU STANDARD; PRT; 11 AA.

AC P42989;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Substance P-like peptide I (PG-SPI).

OS Pseudophryne guentheri (Guenther's toadlet).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;

OC Myobatrachinae; Pseudophryne.

OX NCBI_TaxID=30349;

RN [1]

RP SEQUENCE.

RC TISSUE=Skin secretion;

RX MEDLINE=90287814; PubMed=2356157;

RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,

RA Roberts J.D., Melchiorri P., Erspamer V.;

RT "Six novel tachykinin- and bombesin-related peptides from the skin of
RT the Australian frog Pseudophryne guentheri.";

RL Peptides 11:299-304(1990).

CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Skin.

CC -!- SIMILARITY: Belongs to the tachykinin family.

DR PIR; E60409; E60409.

DR InterPro; IPR002040; Tachy_Neurokinin.

DR InterPro; IPR008215; Tachykinin.

DR Pfam; PF02202; Tachykinin; 1.

DR SMART; SM00203; TK; 1.

DR PROSITE; PS00267; TACHYKININ; 1.

KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;

KW Pyrrolidone carboxylic acid.

FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

FT MOD_RES 11 11 AMIDATION.

SQ SEQUENCE 11 AA; 1294 MW; 3A247C2CC9CB1AB7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.2e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6

Db 1 Q 1

RESULT 61

TKN5_PSEGU

ID TKN5_PSEGU STANDARD; PRT; 11 AA.
AC P42990;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Substance P-like peptide II (PG-SPII).
OS Pseudophryne guentheri (Guenther's toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyla; Myobatrachidae;
OC Myobatrachinae; Pseudophryne.
OX NCBI_TaxID=30349;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=90287814; PubMed=2356157;
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RA Roberts J.D., Melchiorri P., Erspamer V.;
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
RT the Australian frog Pseudophryne guentheri.";
RL Peptides 11:299-304(1990).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR PIR; F60409; F60409.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR InterPro; IPR008215; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1293 MW; 3A247C2CC9CB1457 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.2e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6
 |
Db 1 Q 1

RESULT 62

TKNA_CHICK

ID TKNA_CHICK STANDARD; PRT; 11 AA.

AC P19850;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Substance P.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Intestine;
 RX MEDLINE=88204263; PubMed=2452461;
 RA Conlon J.M., Katsoulis S., Schmidt W.E., Thim L.;
 RT "[Arg3]substance P and neurokinin A from chicken small intestine."
 RL Regul. Pept. 20:171-180(1988).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; JN0023; JN0023.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1377 MW; 21487FE3C9D6C6C7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.2e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 R 5
 |
 Db 1 R 1

RESULT 63

TKNA_GADMO

ID TKNA_GADMO STANDARD; PRT; 11 AA.
 AC P28498;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Substance P.
 OS Gadus morhua (Atlantic cod).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
 OX NCBI_TaxID=8049;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=92298992; PubMed=1376687;

RA Jensen J., Conlon J.M.;
 RT "Substance-P-related and neurokinin-A-related peptides from the brain
 RT of the cod and trout.";
 RL Eur. J. Biochem. 206:659-664(1992).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; S23306; S23306.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR InterPro; IPR008215; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
 FT MOD_RES 11 11 AMIDATION (BY SIMILARITY).
 SQ SEQUENCE 11 AA; 1315 MW; 214860D759D6C6C7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.2e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 K 2
 |
 Db 1 K 1

RESULT 64

TKNA_HORSE

ID TKNA_HORSE STANDARD; PRT; 11 AA.
 AC P01290;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Substance P.
 GN TAC1 OR NKNA OR TAC2 OR NKA.
 OS Equus caballus (Horse), and
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796, 10141;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=Horse;
 RA Studer R.O., Trzeciak A., Lergier W.;
 RT "Isolation and amino-acid sequence of substance P from horse
 RT intestine.";
 RL Helv. Chim. Acta 56:860-866(1973).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=C.porcellus;
 RX MEDLINE=90044685; PubMed=2478925;
 RA Murphy R.;
 RT "Primary amino acid sequence of guinea-pig substance P.";
 RL Neuropeptides 14:105-110(1989).

CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; A01558; SPHO.
 DR PIR; A60654; A60654.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR InterPro; IPR008215; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1349 MW; 3E757FE3C9D6C6C7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.2e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 R 5
 |
 Db 1 R 1

RESULT 65

TKNA_ONCMY

ID TKNA ONCMY STANDARD; PRT; 11 AA.
 AC P28499;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Substance P.
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=92298992; PubMed=1376687;
 RA Jensen J., Conlon J.M.;
 RT "Substance-P-related and neurokinin-A-related peptides from the brain
 RT of the cod and trout."
 RL Eur. J. Biochem. 206:659-664(1992).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; S23308; S23308.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR InterPro; IPR008215; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.

DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
FT MOD_RES 11 11 AMIDATION (BY SIMILARITY).
SQ SEQUENCE 11 AA; 1358 MW; 214860DEC9D6D1F7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.2e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 K 2
|
Db 1 K 1

RESULT 66

TKNA_RANCA

ID TKNA_RANCA STANDARD; PRT; 11 AA.
AC P22688;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ranatachykinin A (RTK A).
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Brain, and Intestine;
RX MEDLINE=91254337; PubMed=2043143;
RA Kozawa H., Hino J., Minamino N., Kangawa K., Matsuo H.;
RT "Isolation of four novel tachykinins from frog (Rana catesbeiana)
RT brain and intestine.";
RL Biochem. Biophys. Res. Commun. 177:588-595(1991).
RN [2]
RP SEQUENCE.
RC TISSUE=Intestine;
RX MEDLINE=94023216; PubMed=8210506;
RA Kangawa K., Kozawa H., Hino J., Minamino N., Matsuo H.;
RT "Four novel tachykinins in frog (Rana catesbeiana) brain and
RT intestine.";
RL Regul. Pept. 46:81-88(1993).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR PIR; A61033; A61033.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR InterPro; IPR008215; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 11 11 AMIDATION.

SQ SEQUENCE 11 AA; 1311 MW; 200D60CC59D40AB7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.2e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 K 2
|
Db 1 K 1

RESULT 67

TKNA_SCYCA

ID TKNA_SCYCA STANDARD; PRT; 11 AA.
AC P41333;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Substance P.
OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
OC Scyliorhinidae; Scyliorhinus.
OX NCBI_TaxID=7830;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=93292508; PubMed=7685693;
RA Waugh D., Wang Y., Hazon N., Balment R.J., Conlon J.M.;
RT "Primary structures and biological activities of substance-P-related
RT peptides from the brain of the dogfish, Scyliorhinus canicula.";
RL Eur. J. Biochem. 214:469-474(1993).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR PIR; S33300; S33300.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1278 MW; 214860DEC9D6D867 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.2e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 K 2
|
Db 1 K 1

RESULT 68

TKN_PHYFU

ID TKN_PHYFU STANDARD; PRT; 11 AA.

AC P08615;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Physalaemin.
 OS Physalaemus fuscumaculatus (Neotropical frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Leptodactylidae;
 OC Leptodactylinae; Physalaemus.
 OX NCBI_TaxID=8378;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=66076612; PubMed=5857249;
 RA Erspamer V., Anastasi A., Bertaccini G., Cei J.M.;
 RT "Structure and pharmacological actions of physalaemin, the main
 RT active polypeptide of the skin of Physalaemus fuscumaculatus."
 RL Experientia 20:489-490(1964).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; S07201; S07201.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1283 MW; 3293693E59C33457 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.2e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6
 |
 Db 1 Q 1

RESULT 69

UF05_MOUSE

ID UF05_MOUSE STANDARD; PRT; 11 AA.
 AC P38643;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Unknown protein from 2D-page of fibroblasts (P48) (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]

RP SEQUENCE.
 RC TISSUE=Fibroblast;
 RX MEDLINE=95009907; PubMed=7523108;
 RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
 RT "Separation and sequencing of familiar and novel murine proteins
 RT using preparative two-dimensional gel electrophoresis.";
 RL Electrophoresis 15:735-745(1994).
 CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
 CC protein is: 5.5, its MW is: 48 kDa.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1328 MW; E54835E5CAAABAFa CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.2e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 K 2
 |
 Db 1 K 1

RESULT 70

ULAG_HUMAN
 ID ULAG_HUMAN STANDARD; PRT; 11 AA.
 AC P31933;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Unknown protein from 2D-page of liver tissue (Spot 118) (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=94147969; PubMed=8313870;
 RA Hughes G.J., Frutiger S., Paquet N., Pasquali C., Sanchez J.-C.,
 RA Tissot J.-D., Bairoch A., Appel R.D., Hochstrasser D.F.;
 RT "Human liver protein map: update 1993.";
 RL Electrophoresis 14:1216-1222(1993).
 CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
 CC protein is: 5.5, its MW is: 34 kDa.
 DR SWISS-2DPAGE; P31933; HUMAN.
 DR Siena-2DPAGE; P31933; -.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1219 MW; EDABD37F272DDB0A CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.2e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6
 |
 Db 3 Q 3

Search completed: April 8, 2004, 15:47:19
Job time : 6.15385 secs